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Post-processing: Minifium Match 0%
Maxifium Match 100%
Listing first 45 summaries
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Maximum DB seq length; 2000000000
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mangifera indica A Carica papaya ACC	Broccoli ACC synth Ananas comosus ACC	1-aminocyclopropan 1-aminocyclopropan	PCR primer #1 used Arabidopsis thalia	ACC synthase gene	Description

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		₽.	ALIGNMENTS	AAD04543	AAQ15133	AAD04545	AAV15705	ABL09570	AAQ63241	AAF23621	AAD04544	AAV15704	AAV20947	AAV31482	AAV30326	AAT73502	ARI,09571	AAQ15135	AAV09713	AAQ15139	AAQ15137	AAQ15138	AAQ15134	AAF23618	AAV13/U1	AAQ15131	AAQ25896	AAT33136	624	726	ААТ72629
				Zucchini CP-ACC 1B	Ċ	1-aminocyc	Genomic clone LE-A	Drosophila melanog	Crucifer 1-aminocy		Tomato 1-aminocycl	Tomato ACC synthas	Mung bean ACC synt	Papaya ACC synthas	Pelargonium 1-amin	Poplar 1-aminocycl	Tomato 1-aminocycl	Clone ptACC2 encod	ynthase	Clone ptaccs encod	PtACC4	ptAcc5	Clone ptACC1 encod	Zucchini ACC synth		Clone pACC1 encodi		ccoli ACC synt	ACC synthase GAC-2	- C	

AAV.	ANV 3 U 3 Z O
ID	AAV30328 standard; DNA; 23 BP.
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DT	28-SEP-1998 (first entry)
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DE	ACC synthase gene PCR primer I.
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ΚW	ACC synthase; 1-aminocyclopropane-1-carboxylate synthase:
KW	ethylene; transgenic plant; wilting; geranium; rose; PCR;
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FH	Key Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ranu
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                                    09-MAY-2000;
12-OCT-2000;
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                                                                                                                                                                                                                                                                                                                       Pelargonium x hortorum
                                                                                                                                                                                                                                                                                                                                                                                      gPHSacc49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Geranium; 1-aminocyclopropane-1-carboxylate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer
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Sacc49; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 BP; 0 A; 2 C; 7 G; 4 T;
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                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of promoter DNA from geranium (Pelargonium x hortorum) genomic clone PHSacc49 (gPHSacc49). This promoter represents the ACC (1-aminocyclopropane-1-carboxylate) synthase gene promoter. The promoter is useful to regulate the transcription level of a coding sequence in geranium and other plants. The present sequence represents a PCR primer used to amplify a DNA fragment of geranium PHSacc genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New
of g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ranu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COLS ) UNIV COLORADO STATE (TAGA-) TAGAWA GREENHOUSES !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                               stress; metabolic pathway; biosynthetic insecticide; antibiotic; ds.
                                                                                                                                                                                                                                                                                 Arabidopsis thaliana; thale cress;
                                                                                                                                                                                                                                                                                                    Arabidopsis
                                                                                                                                                                                                                                                                                                                       21-AUG-2002
                                                                                                                                                                                                                                                                                                                                        ABQ65439;
                                    (HAAS/)
(GARC/)
                                                      (MATH/)
(LEDF/)
(WOES/)
                                                                                                                                                                                                                           US2002059663-A1
                                                                                                                                                                                                                                             Arabidopsis thaliana
                 (KRIC/)
                                                                                 (RAME/)
(PAGE/)
                                                                                                     (RAIN/)
                                                                                                                               (ANYY/)
                                                                                                                                                                     27-JAN-2000; 2000US-178506P
                                                                                                                                                                                       26-JAN-2001; 2001US-0770149
                                                                                                                                                                                                         16-MAY-2002
                                                                                                                        (PRIC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      geranium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGNYTNCCNGGNTTYMGNRTNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-075241/10
                                                                                                                                                                                                                                                                                                                                                                                                         GGNYTNCCNGGNTTYMGNRTNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Fig
LEDFORD B L.
WOESSNER J P.
HAAS W D.
GARCIA C A.
KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 23; Conserv
                                                                                                      YU Y
                                                                        PAGE A.
MATHEW A V.
                                                                                                                                HAMILTON C M
                                                                                                                                          ΑN
                                                                                          RAMEAKA J G
                                                                                                              RAINES T M.
                                                                                                                        PRICE J L.
                                                                                                                                                  GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oter from the 1-aminocyclopropane-1-carboxylase synthase geneium, useful to regulate level of transcription of coding in geranium and other plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           67.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                    thaliana polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; 38pp;
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 2 C; 7 G; 4 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                            748
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.4;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                       plant; transgenic; GMO; (
hetic pathway; nutrition;
                                                                                                                                                                                                                                                                                                     SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24;
1.1e+02;
es 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                          fungicide;
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(DAVI/)

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Вb
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                               l-aminocyclopropahe-1-carboxylic acid; ACC synthase; p flowering; inhibition; regulation; development; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (AB065424-AB066422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, nosecticides and antibiotics).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at segdata.uspto.gov/sequence.html?DocID=999999770149.
                                                                                                                intron
                                                                                                                                                                                                                                             Ananas
                                                                                                                                                                                                                                                                                                  1-aminocyclopropane-1-carboxylic acid synthase gene acacc3.
                                                                                                                                                                                                                                                                                                                                 08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                          AAV00220;
                                                                                                                                                                                                                                                                                                                                                                               AAV00220 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ II 10 16; 40pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistance or altered metabólism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 748 BF; 209 A; 202 C; 120 G; 213 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorlach J, An Y, Ham. Rameaka JG, Puge A, Y Garcia CA, Kricker M, Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HOFF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCTTCCTGGTTTCCGCGTGGG 595
                                                                                                                                                                                                                                           comosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 67.0%;
1 Similarity 56.5%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HURBAN P
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                     /*tag= a
/product= "acacc3"
/pote= "no stop cod
1..101
/*tag= b
                                               /3umber= 1
132.193
/*tag= c
/pumber= 1
194.961
/*tag= d
/number= 2
                                                                                                                                                                                                      Location/Qualifiers
1..961
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                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamilton CM, Price JL, Raines TM, A, Mathew AV, Ledford BL, Woessner T M, Slater T, Davis KR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                 961
                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; Di
Pred. No. 1.5e-
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                           codon given; contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5e+02;
6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu Y;
JP, Haas WD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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06-NOV-1997 AU9719963-A.

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RESULT 5
AAVOUZLT 5
AAVOUZLT 6
AX AAVO
XX AAVO
DT 08-J
XX 1-am
XX 1-am
XX FH Key
FT CDS
FT CDS
FT CDS
FT FT
FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the nucleotide sequence encoding a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of pineapple. The present invention describes a transgenic variety of pineapple in which initiation of flowering is inhibited, the variety of pineapple in which initiation of flowering is inhibited, the variety comprising a nucleotide sequence encoding an ACC synthase enzyme where the nucleotide sequence is operably linked, in the sense or antisense orientation, to one or more regulatory nucleotide sequences. The ACC synthase gene can be used to regulatory nucleotide sequences, the ACC particularly for inhibiting initiation of flowering. Such plants can then be induced to flower in a narrow spectrum of time which would thereby decrease the spread of fruit maturity within a crop.
                          01-MAY-1996;
                                                                                     01-MAY-1997;
                                                                                                                                                 06-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ananas comosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
flowering; inhibition; regulation; development; fruit; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-aminocyclopropane-1-carboxylic acid synthase gene acacc2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV00219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 961 BP; 235 A; 246 C; 247 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 2; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GOLD-)
(QUEE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGNYTNCCNGGNTTYMGNRTNGG 23
|| :| || || ||::| :| ||
567 GGGCTACCAGGCTTTCGCGTCGG 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Botella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1998-009279/02.
DB; AAW37445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 67.0%;
Il Similarity 56.5%;
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J, Sanewski G;
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STATE QUEENSLAND.
UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                          96AU-0009582
                                                                                  97AU-0019963
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                                                                                                                                                                                                                                                          /*tag= a
/product= "acacc2"
/transl_except= (pos:967..968,aa:Val)
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.4; DB 19;
Pred. No. 1.5e+02;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             961;
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0;

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RESULT 6
AAT33139
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the nucleotide sequence encoding a l-aminocyclopropane-l-carboxylic acid (ACC) synthase enzyme of pineapple. The present invention describes a transgenic variety of pineapple in which initiation of flowering is inhibited, the variety comprising a nucleotide sequence encoding an ACC synthase enzyme where the nucleotide sequence is operably linked, in the sense or antisense orientation, to one or more regulatory nucleotide sequences. The ACC synthase gene can be used to regulate pineapple plant development, particularly for inhibiting initiation of flowering. Such plants can then be induced to flower in a narrow spectrum of time which would thereby decrease the spread of fruit maturity within a crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated ACC synthase genes from pineapples - used to generate transgenic pineapples in which the natural initiation of flowering is inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOLD-)
                                                                                                                                                                                                                                                                     ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase; ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
                                                                                                                                                                                                                                                                                                        Broccoli
                                                                                                                                                                                                                                                                                                                                                                               AAT33139 standard; cDNA; 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Botella J,
                                                                                                                                                                                                                                                                                                                                 07-DEC-1996
                                                                                                                                                                                                                                                                                                                                                       AAT33139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYQU)
                                             07-JUN-1995;
                                                                                            WO9621027-A1
                                                                                                                                         primer_bind
                                                                                                                                                                           primer_bind
                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                    Brassica oleracea
(ASGR-) ASGROW
                       30-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                 571 GGCCTCCCCGGTTTTAGGGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig
                                                                                                                                                                                                                                                                                                         ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  968 BP; 241 A; 235 C; 294 G; 198 T; 0 other;
                                                                                                                                                                                                                                                            broccoli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sanewski G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                        synthase cDNA clone TA13.
                                                                                                                                                                                                                                                                                                                                (first entry)
SEED CO
                       94US-0366992
                                              95WO-US07271
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                                                                                                                                           /note= "primer RMM494"
975..993
                                                                                                                                                                           complement (1..14)
                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                              /*tag=
                                                                                                                                                                /*tag=
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56.5%;
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                                                                                                                  "primer RMM491'
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                                                                                                                                                                                                                                                                                                                                                                                                                                          593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 968;
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RESULT 7
AAT72628
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AAT7
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brassica oleracea cDNA clone TA13 (AAT33137) codes for 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase) (AAR98599), an enzyme involved in ethylene biosynthesis. It was obtd. by PCR amplification (see also AAT33140) of broccoli floret cDNA. The PCR product was cloned into pCR11 to obtain clone TA31. cDNA or genomic DNA (see also AAT33136) can be inserted, in sense or antisense orientation, into an expression cassette and then transferred to a binary vector suitable for Agrobacterium-mediated plant transformation. The constructs permit control of the level of ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis melo) and hence a control of maturation, ageing and shelf-life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of Brassica oleracea - used to regulate ethylene-dependent processes
                                                                                                                                                                                                                                                                                              ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; acaccl; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; pineapple; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boeshore ML,
                                                                                                                                                                                                                                                                                                                                                             Ananas
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT72628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                               AAT72628;
                                              02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                                         Ananas
                       (UYQU ) UNIV
                                                                                    20-SEP-1996;
                                                                                                              27-MAR-1997
                                                                                                                                       WO9711166-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants, esp. to improve shelf life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGNYTNCCNGGNTTYMGNRTNGG
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)B; AAR98599.
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13; Conserv
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                        QUEENSLAND
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                                                                                                                                                                                                                                                                                                                                                             ACC
                                                 96AU-0009603
95AU-0005559
                                                                                       96WO-AU00591
                                                                                                                                                            /product= acaccl
/product= acaccl
/EC_number= 4.4.1.14
/note= "Sequence represents 75% of the coding
/note= "Sequence and does not contain the star
                                                                                                                                                                                                                                       1..1080
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50pp; English.
                                                                                                                                                                                                                                                                                                                                                             synthase,
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56.5%;
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                                                                                                                                                                                                                                                                                                                                                               acacc1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reynolds JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruttencutter GE;
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Botella

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RESULTY
AAT7263
ID 768
XXX AAT7263
XXX AAT
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  WPI; 1997-202875/18
P-PSDB; AAW18289.
                                                                                                                                                                    02-MAY-1996;
20-SEP-1995;
                                                                                                                     (UYQU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC synthase; S-édenosyl-L-methionine methylthioadenosine lyase; miaccl; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; mango; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a novel gene, acacci, which encodes an ACC synthase. The enzyme ACC synthase is involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechan.cal wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mangifera
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|| :| || || || ::| :| ||
91 GGTCTCCCCCGATTCCGAGTCGG 71:
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                                                                                                                        VIND
                                                                        JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indica
                                                                                                                                                                                                                                                                               /*tag= a
/product= miaccl
/EC_number= 4.4.1.14
/EC_number= 8.4.1.14
/note= "Sequence represents 75% of the codiny
requence and does not contain the start
or stop codons."
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                                                                                                                     QUEENSLAND.
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35AU-0005559
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56.5%;
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4; Mismatches
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Pred. No. 1
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving storage life.

Sequence 1096 BP; 302 A: 227 ~ ~-
 Pineapple,
therapy to
                                WPI; 1997-202875/18
P-PSDB; AAW18288.
                                                                                                                                                                                                                                                                                                                       ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; capacc2; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; papaya; multigene family; ss.
                                                                                                          02-MAY-1996;
20-SEP-1995;
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therapy to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGNYTNCCNGGNTTYMGNRTNGG 23
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                                                                                                                                                                                                                                                                                                       papaya.
                                                                                                                                                                                                                                                                                                                                                                               papaya
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papaya and mango ACC synthase genes produce fruits with reduced senescer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papaya and mango ACC synthase genes - used
produce fruits with reduced senescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                     QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                               ACC synthase
                                                                                                         96AU-0009603
95AU-0005559
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/EC_number= 4.4.1.14
/product= capacc2
/note= "Sequence represents 75% of the cod sequence and does not contain the or stop codons."
                                                                                                                                        96WO-AU00591
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56.5%;
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.6e+02;
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          used
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senescence

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RESULT 10
AAT72629
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                      ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; capaccl; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; papaya; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3;
                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                Carica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reducing senescence and thus improving storage life.
                                 Pineapple, papaya and mango ACC synthase genes - used therapy to produce fruits with reduced senescence
                                                                                                              Botella
                                                                                                                                                              02-MAY-1996;
20-SEP-1995;
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                                                                                                                                                                                                                             27-MAR-1997
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          Claim
                                                                         P-PSDB;
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DB; AAW18287.
          2; Fig
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13; Conserv
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          2; 46pp; English
                                                                                                                                      QUEENSLAND
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                                                                                                                                                                95AU-0005559
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/product= capacc1
/note= "Sequence rep:
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1..1104
                                                                                                                                                                                                                                                                                                                                                /*tag=
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56.5%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1098;
                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 11
AAT72632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a novel gene, capaccl, a member of the papaya ACC synthase multigene family. ACC synthase is an enzyme involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence and the particular fruit ripening, reducing senescence and the particular fruit ripening.
                                                                                                                                 WPI; 199
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; miacc2; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; mango; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1104 BP; 325 A; 214 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thus improving storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mangifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mangifera indica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT72632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT72632
This sequence represents the novel gene, miacc2, which is a member of the mango ACC synthase multigene family. ACC synthase an enzyme involved in the pathway for ethylene biosynthesis and the rate of
                                                                                        Pineapple,
therapy to
                                                                                                                                                                                                                                      02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                                                                                                          W09711166-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697
                                                           Claim 5; Fig 5; 46pp; English
                                                                                                                                                                             Botella
                                                                                                                                                                                                      (UYQU ) UNIV
                                                                                                                                                                                                                                                                                20-SEP-1996;
                                                                                                                                                                                                                                                                                                             27-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATTCCCTGGATTTAGAGTTGG 719
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                                                                                                                                 1997-202875/18.
DB; AAW18290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      indica
                                                                                      papaya and mango ACC synthase genes - used produce fruits with reduced senescence % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                         QUEENSLAND
                                                                                                                                                                                                                                    96AU-0009603
95AU-0005559
                                                                                                                                                                                                                                                                                96WO-AU00591
                                                                                                                                                                                                                                                                                                                                                                                              /product= miacc2
/note= "Sequence represents 75% of the coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC
                                                                                                                                                                                                                                                                                                                                                                                                                              /EC_number= 4.4.1.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.0%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase miacc2 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                                                                       or stop codons."
                                                                                                                                                                                                                                                                                                                                                                                     sequence and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.4; DB 18; pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 G; 308 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                     does not contain the start
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RESULT 12
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                      2 DNA sequences (AAT66246-47) respectively code for 1-aminocyclopropahe carboxylage synthases (ACC synthase) GAC-1 (AAW09878) and GAC-2 (AAW09878), enzymes involved in the biosynthesis of ethylene in plants. In a method for the commercial production of transgenic plants, Agrobacterium vectors carrying antisense to inoculate periole explants of amother plant, pref. Pelargonium x domysticum. The resulting callus is cultured and used to regenerate transgenic plants. The antisense genes for ACC synthase or ACC oxidase (see also AAT66248) are used to regenerate transgenic plants. The antisense genes prevent ACC synthase or ACC oxidase expression and hence ethylene formation and fruit ripening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either same or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senes:eace and thus improving storage life.
                                                               Sequence 1170 BF; 319 A; 263 C; 297 G; 291 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; Page 24; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Commercial propagation of transgenic plants by tissue culture - especially Pelargonium x domesticum with decreased ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC synthase; 1-gminocyclopropane-1-carboxylate synthase; antisense; ethylene; transgépic plant; Pelargonium x domesticum; in vitro propagation; tissue culture; ripening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT66247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OGLE-) OGLEVEE LITD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC synthase GAC-2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT66247 standerd; DNA; 1170 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 GGGTTCCCACGCTTTAGGGTCGG 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-281013/25.
DB; AAW09873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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56.5%;
67.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
Score 15.4;
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Pred. No. 1.
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DB 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stoots E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
Length 1170;
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Matches 13; Conserv
Brassica oleracea genomic clone ACCA1 (AAT33136) codes for 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase) (AAR98598), an enzyme involved in ethylene biosynthesis. It was obtd. by subjecting broccoli leaf total genomic DNA to PCR using primers (see also AAT33137-38) based on the Arabidopsis thaliana ACC synthase gene. The product was cloned into pCRII to obtain clone ACCA1. Genomic DNA (see also AAT33139) can be inserted, in sense or antisense orientation, into an expression cassette and then transferred to a binary vector suitable for Agrobacterium-mediated
                                                                                                                                            DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of Brassica oleracea - used to regulate ethylene-dependent processes in plants, esp. to improve shelf life
                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antisense; broccoli;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Broccoli ACC synthase genomic DNA clone ACCAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1996
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                                                                                                                       Claim 2; FiglA-B; 50pp; English.
                                                                                                                                                                                              P-PSDB; AAR98598
                                                                                                                                                                                                          WPI; 1996-334002/33.
                                                                                                                                                                                                                                Boeshore ML,
                                                                                                                                                                                                                                                        (ASGR-) ASGROW SEED CO
                                                                                                                                                                                                                                                                               30-DEC-1994;
                                                                                                                                                                                                                                                                                                                              11-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                        WO9621027-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase;
ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT33136;
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                                                                                                                                                                                                                               Carney KJ,
                                                                                                                                                                                                                                                                               94US-0366992.
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595..1
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432..5
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1352..
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135..4
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                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/note= "primer RMM394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start= 2..4
38..134
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.431
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                                                                                                                                                                                                                               Deng RZ,
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                                                                                                                                                                                                                               Reynolds JF,
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6;
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RESULT 15
AAQ15131
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                                                                                                                                                             Matches
                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                         acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA library prepd. from Cucurbita maxima max EC4.4.1.14 obtd. from cDNA library clones was screened by an antibody method to identify colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/pCMW33. Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant transformation. The constructs permit control of the level of ACC synthase in a transgenic plant (esp. B. oleracea or Cucumis melo) and hence a control of maturation, ageing and shelf-life.
AAQ15131;
                           AAQ15131 standard; cDNA; 1703
                                                                                                                                                                                                                   Sequence 1482 BP; 415 A; 341 C; 344 G; 382 T; 0 other;
                                                                                                                                                                                                                                               controls the growth, maturing and aging of higher plants.
                                                                                                                                                                                                                                                                                                                  The gene encoding detriment induced 1-aminocyclopropane-1-carboxylic acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA acid (ACC) synthetase (EC 4.4.1.14) was obtd. by screening a cDNA
                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                        Detriment induced ACC synthetase gene - used for control of bio-synthesis of ethylene, for controlling growth, maturity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-aminocyclopropane-1-carboxylic acid synthetase; detriment;
ethylene; growth; maturity; aging; plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                            ageing of higher plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAR25406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cucurbita maxima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACC synthetase gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ25896 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-253389/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUMO ) SUMITOMO CHEM CO LTD
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56.5%;
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                                                                                                                                                          Score 15.4; DB 13;
Pred. No. 1.6e+02;
4; Mismatches 6;
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Pred. No. 1.6e+02;
4; Mismatches 6;
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Search completed: March 10, Job time: 179.5 secs

2003, 05:25:14

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В
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                                                                                                                  Query Match
Best Local Similarity
                                                         Matches
                                                                                                                                        The ACC synthase cDNA was isolated from C.pepo using a novel method. • A cDNA expression library was prepared from induced plant tissue. The library was screened with an antibody preparation obtained by partially purifying the induced ACC synthase and using it to immunise a suitable mammal. Immunoreactive clones were isolated and sequenced. One of these, pACCl, contained an open reading frame corresponding to a protein of 493 amino acids and mol. wt. 55.779 kD. See also AAQ15132-Q15140.

(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                               Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                              DNA encoding ACC synthase - used for control of plant development and for prodn. of ACC synthase, ethylene and ethanol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone pACC1 encoding the Zucchini ACC synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-DEC-2001
09-MAR-1992
                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1B; 73pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1990;
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854 GGCCTCCCTGGTTTTCGAGTTGG 876
                           GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                         1991-368895/50
                                                         Conservative
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(first entry)
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56.5%;
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                                                                       Score 15.4; DB 12
Pred. No. 1.6e+02;
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     AAV30329
AAS19699
ABG65439
AAT38897
AAT72630
AAT72629
AAH77094
AAT66247
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ACC synthase gene
PCR primer #2 used
Arabidopsis thalia
Carnation ACC synt
Mangifera indica A
Carica papaya ACC
Carica papaya ACC
Human ATP-dependen
ACC synthase GAC-2
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58	58	24	7244	7244	7241	5613	3438	2678	2230	2230	2230	2088	1945	1942	1934	1923	1888	1878	1868	1818	1818	1800	1793	1783	1781	1780	1775	1743	1712	1712	1703	1703	1703	1703	1482	
19	12	22	22	19	12	15	20	19	22	22	19	19	19	17	18	21	19	19	18	22	12	19	12	12	12	12	12	19	22	20	22	22	19	12	13	
AAV15703	AAQ15133	AAF23622	AAD04545	AAV15705	AAQ15140	AAQ63241	AAX35671	AAV30325	AAF23621	AAD04544	AAV15704	AAV20947	AAV30324	AAT38896	AAT66246	AAZ94267	AAV31482	AAV30326	AAT73502	AAD04546	AAQ15135	AAV09713	AAQ15139	AAQ15136	AAQ15137	AAQ15138	AAQ15134	AAV30330	AAS09901	750	S)	AAD04541	AAV15701	AAQ15131	AAQ25896	
ACC	ni AC	ACC syntha		Tomato ACC synthas	Genomic clone LE-A	Crucifer 1-aminocy	DNA encoding a 1-a	oniun	ACC syntha	1-ami	Tomato ACC synthas	Coffee-fruit speci	Pelargonium 1-amin	ation ACC syn	ynthase (bean ACC syn	Papaya ACC synthas	nium 1-ami	1-aminocyc	1-amin	e ptACC2	ynthase	ptACC6	PtACC3	ptAcc	_	Clone ptACC1 encod	Rose 1-aminocyclop	DNA encoding 1-ami	Banana 1-aminocycl	AC	1-am	ucchini ACC	ne pACC1 encc	ACC synthetase gen	

ALIGNMENTS

AAV30329 standard; DNA; 23 BP

RESULT 1
AAAV30329
ID AAV3
XX AV3
XX AV3
AC AAV3
AC AACC
XX ACC
X Synthetic.
Pelargonium
Rosa sp. Key modified_base modified_base modified_base modified_base ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; ethylene; transgenic plant; wilting; geranium; rose; PCR; ACC synthase gene PCR primer II. modified_base 28-SEP-1998 AAV30329; × (first entry) hortorum /*tag= c /mod_base= 15 /*tag= d /mod_base= 18 /*tag= b /mod_base= /*tag= a /mod_base= Location/Qualifiers primer;

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RESULT 2
AAS19699
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                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                               Primer II and primer I (see AAV30328) were used in PCR amplifications to develop PCR probes for the isolation of geranium and rose 1-aminocycloproane-1-carboxylate synthase (ACC synthase) cDNA clones (see AAV30324-26 and AAV30330). The invention relates to the use of antisense fragments of these genes to control ACC synthase expression in plants. By reducing the amount of ACC synthase produced in plant cells, the rate of ACC conversion to ethylene can be decreased. This can be used to prolong the shelf-life of cut flowers and to reduce leaf yellowing and petal abscission
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced ethylene levels, for increasing shelf-life
       (COLS ) UNIV COLORADO STATE. (TAGA-) TAGAWA GREENHOUSES I
                                09-MAY-2000;
12-OCT-2000;
                                                         09-MAY-2001;
                                                                                          WO200185754-A1
                                                                                                           Pelargonium x hortorum
                                                                                                                                   Geranium; 1-aminocyclopropane-1-carboxylate synthase ACC synthase; plant transcription regulation; plant;
                                                                                                                                                             PCR primer
                                                                                                                                                                                                               AAS19699 standard; DNA;
                                                                                                                                                                                                                                                                                                                         $equence 23 BP; 5 A; 5 C; 0 G; 1 T; 12 other;
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                                                                                                                                                                                               AAS19699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1997;
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                                                                                                                             synthase; plant 
Sacc49; ss.
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                                2000US-203021P.
2000US-239782P.
                                                         2001WO-US15023
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Pred. No.
                                                                                                                                                            DNA fragment of geranium
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PCR; primer;
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(SLAT/)
                                                        (HAAS/)
(GARC/)
                                                                                                                           (PRIC/)
(RAIN/)
                                                                                                                                                                                                                                                                         Arabidopsis thaliana; thale stress; metabolic pathway; l
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LEDFORD B L MATHEW A V. PAGE A. RAMEAKA J G YU Y

WOESSNER J P.
HAAS W D.
GARCIA C A.

(MATH/) (PAGE/) (RAME/) (/スススロス)

PRICE J L. RAINES T M.

HAMILTON C M AN Y GORLACH J.

(ANYY/)

(HURB/)

HOFF/

KRICKER M.
SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.

27-JAN-2000; 2000US-178506P 26-JAN-2001; 2001US-0770149 16-MAY-2002 US2002059663-A1 Arabidopsis thaliana insecticide;

antibiotic;

pathway; bi

e cress; plant; biosynthetic p

t; transgenic; GMO; (
pathway; nutrition;

GMO; disease;

fungicide;

metabolic

Arabidopsis thaliana polynucleotide

SEQ

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ŏ 16 21-AUG-2002

(first entry)

ABQ65439 standard;

DNA;

748

ВP

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Query Match
Best Local
                                                                             Matches
                                                                                                                                                                                         The present invention relates to the isolation of promoter DNA from geranium (Pelargonium x hortorum) genomic clone PHSacc49 (gPHSacc49) This promoter represents the ACC (1-aminocyclopropane-1-carboxylate) synthase gene promoter. The promoter is useful to regulate the transcription level of a coding sequence in geranium and other plant: The present sequence represents a PCR primer used to amplify a DNA fragment of geranium PHSacc genes.
                                                                                                                                                                                                                                                                                                                                                                                          New promoter from the 1-aminocyclopropane-1-carboxylase synthase of geranium, useful to regulate level of transcription of coding sequence in geranium and other plants
                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                         Claim
1 CANANNCKRAASMANCCNRSYTC 23
                                    1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-075241/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS
                                                                                                                                                                                                                                                                                                                                                     7; Fig 2;
                                                                             l Similarity
23; Conserv
                                                                                                                                                           23
                                                                             Conservative
                                                                                                                                                       BP; 5 A;
                                                                                                                                                                                                                                                                                                                                                     38pp;
                                                                       100.0%; F.
                                                                                                                                                       5 C; 0 G; 1 T;
                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                Score 15.2;
Pred. No. 1
                                                                             Mismatches
                                                                                                                                                           12 other;
                                                                             DB 24;
1.7e+02;
les 0;
                                                                             Indels
                                                                                                                  Length
                                                                             0
                                                                                                                                                                                                                    plants.
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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RESULT 4
AART38897/c
ID AART3888
AC AART3888
AX IO-FEB
AX Carnat
KW Carnat
KW Carnat
KW Carnat
KW UCACC
EN COMMAY
AX COMMAY
AX COMMAY
AX COMMAY
AX CARNA
BY COMMAY
AX CARNA
BY CARNA
BY CALLR-
PA (FLOR-
AX (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                          (ALLR-)
(FLOR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to nucleic acids (I) that hybridise under stringent conditions to any of 999 sequences (ABB65424-ABB66422) or their fragments. (I) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/biosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at sequence.html?DocID=999909770149.
Producing transjebic plants, with reduced climacteric ethylene prodn. - to give flowers and buds, specifically carnations, with increased post-harvest life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorlach J,
Rameaka JG,
Garcia CA,
Hurban P;
                                                                                                WPI; 1996-51868
P-PSDB; AAW0455
                                                                                                                                                                                                                                                                                                                     09-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                              09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dianthus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carnation; 1-aminocyclopentane-1-carboxylic acid synthase; ACC synthase; co-suppression; ethylene; senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful e.g. for preparing transgenic plants with or altered metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9635792-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carnation ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT38897 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 16; 40pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 66.1%;
Local Similarity 47.8%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CANANNCKRAASMANCCNRSYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAACCCTAAACCATCCGACCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002-479224/51.
                                                                                                                                                                        MT;
                                                                                                                                                                                                                                        ALLRAD NO 1 PTY LTD. FLORIGENE INVESTMENTS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          748 BF; 209 A; 202 C; 120 G; 213 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An Y. Hami
, Page A, M
Kricker M,
                                                                                                                                                                                           Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cv. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthase gene fragment.
                                                                                                                      )/51.
                                                                                                                                                                                                                                                                                                                                                              36WO-AU00286
                                                                                                                                                                                                                                                                                                                  35AU-0002862.
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                                                                                                                                                                                           WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sin.
                                                                                                                                                                                           Gutterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2; DB 24;
Pred. No. 2.8e+02;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Price JL, Raines TM,
Ledford BL, Woessner,
Davis KR, Allen K,
                                                                                                                                                                                           , IN
                                                                                                                                                                                           Michael MZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thaliana sequences,
increased resistance
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JP, Haas WD;
Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748;
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RESULT 5
AAT72631/c
ID AAT72631 standard; DNA; 1096
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                           Pineapple,
therapy to
 This sequence
                        Claim
                                                                                                                                                       02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                           ACC synthase: S-adenosyl-I-methionine methylthioadenosine lyase miaccl; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; mango; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A non full-length gene (AAT38897) comprises nucleotides 287-1373 of a 1-aminocyclopentane-1-carboxylic acid (ACC) synthase gene (AAT38896) isolated. from carnation cv. White Sim. It was obtd. by PCR amplification of carnation cDNA using primers (AAT38899-900) based on highly conserved regions of the ACC synthase gene.

Transgenic carnation plants carrying the non full-length gene show reduced prodn. of ACC synthase or ACC synthase-specific mRNA as a result of co-suppression. This leads to decreased climacteric ethylene prodn. by the plant and hence delayed senescence of flowers and buds after cutting, and increased post-harvest life.
                                                                              P-PSDB;
                                                                                       WPI; 1997-202875/18
                                                                                                              Botella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1085 CAAACCCTAAACCACCCTGGCTC 1063
                                                                                                                                 (UYQU ) UNIV
                                                                                                                                                                                      20-SEP-1996;
                                                                                                                                                                                                                                   WO9711166-A1
                                                                                                                                                                                                                                                                                                                                                         Mangifera
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mangifera indica ACC synthase miaccl
                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT72631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1087 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 42-44; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CANANNCKRAASMANCCNRSYTC 23
                    4; Fig 4; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
11; Conser
                                                                              AAW18289
                                                                                                                                                                                                                                                                                                                                                          indica
                                        papaya and mango ACC synthase genes - produce fruits with reduced senescence
                                                                                                                                 QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
 represents
                                                                                                                                                       96AU-0009603
95AU-0005559
                                                                                                                                                                                        96WO-AU00591
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 A; 204 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.18;
 ۵
 novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.2; DB 17;
Pred. No. 3e+02;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 G; 323 T; 0
gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                  gene.
 miacc1,
                                                    - used
 which
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S.
                                                     'n
נם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1087;
                                                                                                                                                                                                                                                                                                                                                                                                             Lyase
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0;

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RESULT 6
AAT72630/c
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  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of an ACC synthase multigene family found in mango. ACC synthase is involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carica papaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT72630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
synthase is rate of endo
                           of the ACC
                                                                                                                                                                      Botella
                                                                                                                                                                                                                         02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                                                                                  W09711166-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carica papaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT72630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reducing
                                      This sequence represents
                                                                 Claim
                                                                                        therapy
                                                                                                      Pineapple,
                                                                                                                                 P-PSDB;
                                                                                                                                                                                              (UYQU ) UNIV
                                                                                                                                                                                                                                                               20-SEP-1996;
                                                                                                                                                                                                                                                                                         27-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.4.1.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANANNCKRAASMANCCNRSYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGACTCTGAACCAACCAGGCTC 1066
                                                                                                                                1997-202875/18.
DB; AAW18288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                              Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1096 BP; 302 A; 227 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   senescence and thus improving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
nce represents a novel gene, capacc2, which is a member synthase multigene family found in papaya. The enzyme is involved in the pathway for ethylene biosynthesis and dogenous expression of ACC synthase is considered to li
                                                                                       papaya and mango ACC produce fruits with 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ylene biosynthesis; transgenic plant; senescence; pression system; plant development; fruit ripening; papaya; multigene family; ss.
                                                                 ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-adenosyl-L-methionine methylthioadenosine lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC synthase capacc2 gene
                                                                                                                                                                                                                         96AU-0009603
95AU-0005559
                                                                                                                                                                                                                                                               96WO-AU00591
                                                              46pp;
                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                 /product= capacc2
                                                                                                                                                                                                                                                                                                                                                                                               /EC_number= 4.4.1.14
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%;
47.8%;
                                                                 English.
                                                                                                                                                                                                                                                                                                                                           "Sequence represents 75% of the coding sequence and does not contain the start or stop codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.2;
                                                                                           reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                      synthase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   storage life.
                                                                                           senescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                       used
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                                                                                                          'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
    to limit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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This sequence represents a novel gene, capaccl, a member of the papaya ACC synthase multigene family. ACC synthase is an enzyme involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC

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99999999
DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2629/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substantially the rate of ethylene production. Endogenous ethylene i often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plant using either sense or antisense expression system may be used to cor the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                      capacol; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening: EC\ 4.4.1.14; papaya; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1098 BP;
                                                                                                                                                                                                                                                                                                                                                                                                   Carica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT72629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT72629 standard; DNA; 1104
                                                                                                                                                                                                          02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                                                  W09711166-A1
                                                                                 Claim
                                                                                                               Pineapple,
                                                                                                                                   P-PSDB; AAW18287
                                                                                                                                                                 Botella
                                                                                                                                                                                                                                          20-SEP-1996;
                                                                                                                                                                                                                                                              27-MAR-1997.
                                                                                                     therapy
                                                                                                                                                                                      (UYQU ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>_</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANANNCKRAASMANCCNRSYTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATACTCTGAACCACCCCGGCTC 1069
                                                                                                                                              1997-202875/18.
                                                                                2;
                                                                                                                                                                                                                                                                                                                                                                                                   papaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          papaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                     ţ
                                                                                                                                                                  JR;
                                                                                Fig
                                                                                                            papaya and mango ACC synthase genes -
                                                                                                     produce fruits with reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                2; 46pp; English.
                                                                                                                                                                                      QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-adenosyl-L-methionine methylthioadenosine lyase;
                                                                                                                                                                                                          96AU-0009603
95AU-0005559
                                                                                                                                                                                                                                           96WO-AU00591
                                                                                                                                                                                                                                                                                                                                     /product= capaccl
                                                                                                                                                                                                                                                                                                                                          /*tag= a
/EC_number= 4.4.1.14
                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      ..1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthase capaccl gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 A; 275 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%;
                                                                                                                                                                                                                                                                                                     "Sequence represents 75% of the sequence and does not contain t or stop codons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.2; DB 1
No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 T; 0 other;
                                                                                                      senescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                used
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                                                                                                                 in
                                                                                                                                                                                                                                                                                                                              coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sgenic plants
used to control
                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                   start
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AAH77094/C
ID AAH77094
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Best L
This sequence represents cDNA encoding human ATP-dependent serine proteinase 31. The protein has a molecular weight of 31 kD. The inven relates to human ATP-dependent serine proteinase 31 (AAG66837), nucle of ATP-dependent serine proteinase 31 kD. The recombinant produc of ATP-dependent serine proteinase 31. The present invention addition discloses an antagonist of ATP-dependent serine proteinase 31 for therapeutic use, and an antibody which specifically binds to ATP-dependent serine proteinase 31. ATP-dependent serine proteinase 31, a nucleotides which encode it may be used for treating a variety of diseases, such as malignant tumours, blood diseases, HTV (human immunodeficiency virus) infection, immune disorders and inflammatory conditions. The protein may also be used to screen for modulators of activity or for paptide fingerprinting identification. The polynucleo
                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenosine triphosphate dependent serine proteinase 31 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumor, hemopathy, human immunodeficiency virus infection, immunological diseases and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ATP-dependent serine proteinase 31; recombinant production; malignant tumour; cancer; blood disease; HIV infection; human immunodeitichency virus; immune disorder; inflammatory condit cytostatic; anti-HIV; antiinflammatory; immunomodulator; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-2000; 200qcn-0115085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1097 CAGACGCTG!ACCAGCCAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SHAN-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-CN00405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH77094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence thus improving storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-626440/72.
                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-dependent serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHANGHAI BIOWINDOW GENE DEV INC
                                                                                                                                                                                                                                                                                                                                                                                        Page 30-31; 36pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%;
47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Human ATP-dependent serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                        Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteinase 31-encoding
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Pred. No. 3e+(
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; DB
3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1104;
            polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condition;
                                                                                                                                                                                                                      nt production additionally
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                                                                                                                                                                                                                                                                          invention
nucleic
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Qy

1 CANANNCKRAASMANCCNRSYTC

Query Match Best Local S Matches 11

Similarity

66.1%; 47.8%;

Score 15.2; DB Pred. No. 3e+02;

DB 18;

1170;

Mismatches

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Indels Length

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Gaps

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Conservative

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RESULT 9
AAT66247/c
ID AAT66247 standard; DNA; 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SXCCC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                      2 DNA sequences (AAT66246-47) respectively code for 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1 (AAW09879) and GAC-2 (AAW09879), enzymes involved in the biosynthesis of ethylene in plants. In a method for the commercial production of transgenic plants, Agrobacterium vectors carrying antisense genes for ACC synthase or ACC oxidase (see also AAT66248) are used to inoculate peticle explants of a mother plant, pref. Petargonium x domesticum. The resulting callus is cultured and used to regenerate transgenic plants. The antisense genes prevent ACC synthase or ACC oxidase expression and hence ethylene formation and fruit ripening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 can be used as probe for hybri microarrays.
  Sequence 1170 BP;
                                                                                                                                                           Claim
                                                                                                                                                                                           Commercial especially
                                                                                                                                                                                                                                                                                 (PENN-)
                                                                                                                                                                                 formation
                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                              Arteca
                                                                                                                                                                                                                                                                                                                    09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                         08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                             ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; ethylene; transgenic plant; Pelargonium x domesticum; in vitro propagation; tissue culture; ripening; ss.
                                                                                                                                                                                                                                                                                                                                                                 15-MAY-1997.
                                                                                                                                                                                                                                                                                                                                                                                     WO9717429-A1
                                                                                                                                                                                                                                                                                                                                                                                                            Not identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT66247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1154 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 CAGAGACGGAAGCAGCCAAGCTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase
                                                                                                                                                                                                                                      1997-281019/25
                                                                                                                                                         14; Page 24; 36pp;
                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
11; Conser
                                                                                                                                                                                                                                                                                 OGLEVEE LTD.
PENN STATE RES
                                                                                                                                                                                                                             AAW09879
                                                                                                                                                                                         propagation of transgenic
Pelargonium x domesticum w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed as a primer for nucleic acid hybridisation reactions, or in
                                                                                                                                                                                                                                                            Arteca RN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                   9508-0555755
                                                                                                                                                                                                                                                                                                                                         96WO-US17954
319 A; 263 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.1%;
47.8%;
                                                                                                                                                                                                                                                                                  FOUND
                                                                                                                                                                                                                                                           Oglevee-O'Donovan
                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; I
Pred. No. 3e+0
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.2; DB
No. 3e+02;
ç;
                                                                                                                                                                                         c plants by tissue culture with decreased ethylene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ç;
 291 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 T;
                                                                                                                                                                                                                                                           ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amplification r producing gene
                                                                                                                                                                                                                                                           Stoots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.
other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reactions
e chips or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     antisense; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
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RESULT 11
AAQ15131/c
ID AAQ151
XX AAQ151
XX AAQ151
XX O9-MAR
DT 17-DEC
DT 09-MAR
XX Clone
XX 1-amin
KW courge
XX Cucurb
XX Cucurb
XX Cucurb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
AAQ25896/c
                                                                                                                                                                                                                                                           В
                                                                                                                                                                                 밁
                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                           The gene encoding detriment induced 1-aminocyclopropane-1-carboxylic acid (ACC) synthetase (EC 4.4.1.14) was obtod by screening a cDNA library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtd. from cDNA library clones was screened by an antibody method to identify colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/pCMW33. Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene controls the growth, maturing and aging of higher plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1163 CAGACTCTGAACCACCCTGGCTC 1141
                                                                                                                                                                                  1244
                                                                                                                                                                                                                                                                                                                                                                      Detriment induced ACC synthetase gene - use
bio-synthesis of ethylene, for controlling
ageing of higher plant
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1992-253389/31.
P-PSDB; AAR25406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ25896 standard; cDNA; 1482
                                                                                                                                                                                                                                                          Sequence 1482 BP; 415 A; 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cucurbita maxima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-aminocyclopropane-1-carboxylic acid synthetase; ethylene; growth; maturity; aging; plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACC synthetase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-1993
                                                                Clone pACC1
                                                                                    17-DEC-2001
09-MAR-1992
                                                                                                                                   AAQ15131 standard;
                                                                                                                                                                                                                                                                                                                                                      Claim 3; Fig 1; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP04169183-A.
                   Cucurbita pepo
                                     courgette;
                                                                                                                AAQ15131;
                                                                                                                                                                                                                                                                                                                                                                                                                                       (SUMO ) SUMITOMO CHEM CO LTD
                                              l-aminocyclopropane-1-carboxylic acid synthase;
                                                                                                                                                                                                                      Local Similarity les 11; Conserv
                                                                                                                                                                                                   1 CANANNCKRAASMANCCNRSYTC
                                                                                                                                                                                 CAAACTCGAAACCAACCTGGCTC 1222
                                      ss.
                                                                encoding the Zucchini ACC synthase
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                   (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           90JP-0296943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90JP-0296943
 Location/Qualifiers
                                                                                                                                   cDNA; 1703
                                                                                    entry)
                                                                                                                                                                                                                              66.18;
47.88;
                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                              Score 15.2;
Pred. No. 3.
                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                            C; 344 G; 382 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВΡ
                                                                                                                                   ВP
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                    3.1e+02;
5;
                                                                                                                                                                                                                                                                                                                                                                                           used for control
                                                                                                                                                                                                                                                                                                                                                                                 ed for control of growth, maturity
                                                fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detriment;
                                                                                                                                                                                                                                        Length 1482;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                           В
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RESULT 12
AAV15701/c
ID AAV15
XX AV15
AC AAV15
AC AAV15
AC AV15
XX 2ucch
XX 2ucch
XX 2ucch
KW 1-ami
KW 1-ami
KW 1-belay
XX Cucur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The ACC synthase cDNA was isolated from C.pepo using a novel method. A cDNA expression library was prepared from induced plant tissue. The library was screened with an antibody preparation obtained by partially purifying the induced ACC synthase and using it to immunise a suitable mammal. Immunoreactive clones were isolated and sequenced. One of these, pACC1, contained an open reading frame corresponding to a protein of 493 amino acids and mol. wt. 55.779 kD. See also AAQ15132-Q15140.
(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1B; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USN7579896-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                             zucchini; courgette; ACC synthase; conserved peptide;
1-aminocyclopropane-1-carboxylic acid synthase;
delayed fruit ripening; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1254 CAAACTCGAAACCAACCTGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theologis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USDA ) US SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1991.
                                                                                                                                                                                                                                                                                                                     01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                               AAV15701 standard; cDNA; 1703
                      US5723766-A
                                                                                                                                                          Cucurbita
                                                                                                                                                                                                                                                                                Zucchini ACC
                                                                                                                                                                                                                                                                                                                                                            AAV15701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding ACC synthase - used for control of plant development for prodn. of ACC synthase, ethylene and ethanol \,
                                                                                                                                                                                                                                                                                                                                                                                                                      ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1991-368895/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR15504
                                                                                                                                                          pepo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                              synthase clone
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF AGRICULTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /EC_number=
1683..1688
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-0579896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0579896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11..1492
/*tag= a
                                                                                                     11..1492
                                                           /product= ACC_synthase
                                                                              /*tag=
                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.1%;
47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.4.1.14
                                                                                                                                                                                                                                                                                pACC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2; DB 12;
Pred. No. 3.2e+02;
- Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                           clone pACC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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В
                                                                                                                                                                                                                                                                                                                                         AAD04541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is the zucchini
1-aminocyclopropane-1-carboxylic acid (ACC) synthase clone pACC1.
pACC1 was used in the isolation of conserved sequences from five tomato (LE-ACC 1A, LE-ACC 1B, LE-ACC 2, LE-ACC3 and LE-ACC4) and two zucchini (CP-ACC 1A) and CP-ACC 1B) ACC synthases.
A novel DNA molecule comprises an expression system which, when contained in a plant host cell, generates RNA that is sufficiently complementary to an RNA transcript of an endogenous ACC synthase gene to prevent its synthesis. The expression system consists of the reverse transcript of the antisense RNA (i.e. cDNA) operably linked to control sequences that effect its transcription into the antisense RNA, where the cDNA can be amplified from the endogenous ACC synthase gene by primer pairs encoding conserved ACC synthase sequences. The DNA molecule can be used to delay ripening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1992;
10-SEP-1990;
25-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                 1254 CARACTCGARACCTGGCTC 1232
   25-JAN-1995;
                                                                                                                                                            Cucurbita pepo.
                                                                                                                                                                                      Zucchini; 1-amino(yclopropane-1-carboxylic acid synthase; pACC1; ethylene production; fruit ripening; transgenic plant; ss.
                                                                                                                                                                                                                                 Zucchini 1-aminoc/clopropane-1-carboxylic acid synthase (pACC1) cDNA
                                                                                                                                                                                                                                                              04-JUL-2001 (f..rst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1703 B?; 481 A; 359 C; 378 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Column's 33-38; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding anti-sense RNA blocking plant ACC synthase expression is used for producing transgenic plants with delayed fruit ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-2060(5/18.
P-PSDB; AAW47310!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato T,
                           27-MAR-2001.
                                                        US6207881-B1.
                                                                                                                                                                                                                                                                                                                         AAD04541 standa::dl: cDNA; 1703 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tomato or zucchini fruits.
                                                                                                                                                                                                                                                                                                                                                                                                                             1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 47.8
ll; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theologis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0862493.
90US-0579896.
95US-0378313.
95US-0481171.
55US-0378313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0481171.
                                                                                 /rag= a
/product= "Zucchini pACC1"
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%;
47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.2;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 19;
1.2e+02;
les 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Дb
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                                                                                                                                                                                                                25-JAN-1995;
02-APR-1992;
07-JUN-1995;
10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a cDNA encoding zucchini (Cucurbita pepo) 1-aminocyclopropane-1-carboxylic acid synthase (pACC1). ACC synthase are capable of catalysing the conversion of AdoMet (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher halfs, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1254 CAAACTCGAAACCAACCTGGCTC 1232
Expression cassette for producing transgenic plants exhibiting inhibited ethylene production and delayed fruit ripening, comprise complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic
                                                                                                                                                                            (USDA ) US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                    02-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucurbita pepo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC synthase; 1-aminocyclopropane-1-carboxylic acid synthase; ethylene production; fruit ripening; enzyme; zucchini; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zucchini ACC synthase clone pACC1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF23618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1703 BP; 481 A; 359 C; 378 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1B; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2 useful for producing ACC synthase which is essential for the production of ethylene in higher plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1992;
10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF23618 standard; DNA; 1703 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Joca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-289591/30.
                                                                             2001-079558/09.
B; AAB59716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ll Similarity 47.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE00980
                                                                                                                                     Theologis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                95US-0378313.
92US-0862493.
95US-0481171.
90US-0579896.
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90US-0579896
                                                                                                                                                                                                                                                                                                                    98US-0033349
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47.8%; Pred. No. 3
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The invention relates to two isolated cDNA molecules ((pASC6) and (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an ethylene forming enzyme (EFE), respectively. The clones are deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814, respectively. pASC6 and pACOS7 may be used to genetically control ethylene biosynthesis in plants and hence regulate the ethylene-induced processes involved in fruit ripening (and other ethylene related processes). Vectors comprising the cDNA sequences may be used to produce transgenic bananas with altered fruit ripening characteristics. The orientation of the pASC6 and pACOS7 used in the construct, will determine the tripening process is affected. If the genes have a sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX27501 standard; cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated cDNA molecules ((pASC6) and (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an eforming enzyme (EFE) - useful for modifying fruit ripening
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Best Local
                                                                                                                                                                 orientation, and transcribe mRNA that encodes an active enzyme, the rate of ripening will be increased (up-regulation) (however, full-length sense constructs can also be used to inhibit enzyme expression by coinhibition). If genes encode antisense mRNA, they will inhibit the expression of the genes involved in fruit ripening and hence slow the process down (down-regulation). In this manner different spatial and temporal patterns of genes expression can be produced. Retardation of the rate of ripening will reduce the rate of deterioration of banana fruit after harvest. This helps in production of high quality fruit that has improved flavour and texture. The present sequence represents the cDNA sequence of the banana ACS enzyme.
 1265
                                                                                                                                    Sequence 1712
                                  1 CANANNCKRAASMANCCNRSYTC
CACACCCTGAACCACCCCGGCTC 1243
                                                                                   Similarity
                                                                     Conservative
                                                                                                                                          B₽;
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47.8%;
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Search completed: March 10, Job time: 173.5 secs

2003, 05:25:16

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Title:
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Maxinum Match 100%
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Maximum DB seq length; 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
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1 gqm/tnccnggnttymgnrtngg
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	RESULT 1 AR050170 LOCUS DEFINITION ACCESSION VERSION VERSION		11111111111111111111111111111111111111	Result No.
P; 1 - R; 1 - G; G;	AR0501 Sequen AR0501 AR0501		11111111111111111111111111111111111111	Score
0 . 8 8 11 11	0170 ence 9 0170 0170.1		67.0 67.0 67.0 67.0 67.0 67.0 67.0 67.0	Query Match
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l-carboxylate s 9 20-OCT-1998; alifiers	23 bp nt US 5824875.	ALIGNMENTS	TOMACCD LEU18058 AB005723 AF146027 AF146027 AF146026 TOMACCC AB0005722 AF146025 TOMACCB TOMACCC PSACCS LEACSIB1	ID
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genes from pelargonium	linear PAT 29-SEP-1999		350170 Sequen 329 Lycopers 3058 Lycopers 3058 Lycopers 305027 Actini 46027 Actini 46027 Actini 46027 Actini 320 Lycopers 322 Lycopers 460 Lycopers 461 Stripa 473 Citrus 4873	Description

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                                                    Lycopersicon (LE-ACS5) DNA U18058
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13; Conser
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Yip,W.K., Moore,T. and Yang,S.F.
Differential accumulation of transcripts for four tomato
Distriction of transcripts for four tomato
Distriction of transcripts for four tomato
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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1-aminocyclopropane-1-carboxylate synthase; homoloc
Lycopersicon esculentum ripe pericarp cDNA to mRNA.
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/protein_id="AAA68623.1"
/db_xref="G:867993"
/translation="EHNHLVCDEIYAATVFNPPKFVSIAEIINEDNCINKDLVHIVS
SLSKDLGFPGFRVGIVYSFNDDVVNCARK"
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2 c 7 g
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/db_xref="taxon:4081"
/tissue_type="pericarp"
/dev_stage="ripe"
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                                                                                                                                                                                                                                                                                                                                                                     /EC_number="4.4.1.14"
/note="homologue"
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Pred. No. 2.1e+03;
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                                                                                            PLN 08-MAR-1997
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Best Local Similarity
Matches 13; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-DEC-1994) Athanasios Theologis, Plant Gene Expression Center, ARS/USDA, 800 Buchanan Street, Albany, CA 94710 and Department of Plant Biology, University of California, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawakita,K., Hennig,L., Lincoln,J.E., Rottmann,W.H., Campbei Zarembinski,T.I., Yu,G.X., Taylor,L.D. and Theologis,A. The tomato 1-aminocyclopropane-1-carboxylate (ACC) synthase musical family is encoded by at least eight members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             multigene family is 
Unpublished
                                                                                                      AB005723.1 GI:2274792
ACC Synthase.
ACC Synthase.
Actinidia deliciosa (sub_species:deliciosa, strain:Hayward)
wound-treated fruit cDNA to mRNA.
Actinidia deliciosa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots
Asteridae; Ericales; Actinidiaceae; Actinidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon.
                 Cloning and expression of genes encoding ACC Acta Horticulturae 398, 179-186 (1995) 2 (bases 1 to 265)
                                                                                                                                                                                                                                                      Actinidia deliciosa mRNA
AB005723
                                                                                                                                                                                                                                                                                          AB005723
                                                                        Ikoma,Y.,
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   (bases 1 to ma, Y.
                                                                                           (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="AGC synthase"
/protein_id="AAB48947.1"
/db_xref="G::1561702"
/tanslation="ILIFAMTKNIHIVSDEIYAGTVFDSPKFVSIIEALIDRKLEKS
KMWNOYHIVSSLSKDLGLFGFRVGMIYSN"
4 1 c 40 g 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cyclopropane-1-carboxylate synthase"
/note="direct precursor of ethylene; one member of a multigene family; from TZ region to the reaction center; similar to the product encoded by PIR Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="converts SAM to ACC; plant hormone biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="LE-ACS5"
<1. .>221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esc
/cultivar="Rutgers"
/db_xref="taxon:4081"
/clone="PSF31 (stock #394)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="LE-ACS5"
/EC_number="4.4.1.14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /standard_name="Lycopersicon esculentum 1-amino-
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                                                                          Yano, M. and Ogawa, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu,C., Cher,D., Chen,K. and Zhang,S. Direct Submission
Submitted (27-APR-1999) Department of Horticulture, Huajiachi
Campus, Zhéjiang University, Kaixuanlu 268, Hangzhou, Zhejian
310029, Fedple's Republic of China
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Submitted (11-JUL-1997) Yoshinori Ikoma, National Institute of Fruit These Science, Department of Citriculture; Okitsu, Shimizu, Shizuoka 424-02, Japan (E-mail yoshino@okt.affrc.go.jp, Tel:+81-543-69-7111, Fax:+81-543-69-2115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinidia ;hinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Aggnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Actinidiaceae; Actinidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases: to 265)
Xu,C., Chen,K., Chen,D. and Zhang,S.
Molecular cloning of four members of ACC synthase gene family from kiwifruit (Actinidia chinensis Planch.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinidia chinensis.
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3ASTYCNRDLIHTVYSLSKDLGFPGFRYGIVYSYNDQVTLCAL"
a : 67 c 50 g 67 t
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<1. .>265
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/strain="Hayward"
/sub_species="deliciosa"
/db_xref="taxon:3627"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /qrganism="Actinidia chinensis"
/db_xref="taxon:3625"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note="ACS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Actinidia chinensis Planch"
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56.5%;
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Score 15.4; DB 8;
Pred. No. 1.6e+03;
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                          Length 265;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                           204 GGTCTCCCGGGTTTCCGGGTCGG 226
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                                                                       1-aminocyclopropane-1-carboxylate synthase; homologue.
Lycopersicon esculentum red ripe fruit pericarp cDNA to mRNA.
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnonlophyta; endicotyledons; core endicots;
Asteridae; enasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu,C., Chen,D., Chen,K. and Zhang,S. Direct Submission Submitted (27-AR-1999) Department of Horticulture, Huajiachi Campus, Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang 310029, People's Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;
Asteridae; Ericales; Actinidiaceae; Actinidia.
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Molecular cloning of four members of ACC synthase gene family from kiwifruit (Actinidia chinensis Planch.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinidia chinensis.
Actinidia chinensis
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AF146026
Yip,W.K., Moore,T. and Yang,S.F.
Differential accumulation of transcripts for four tomato
                                                                                                                                                                                                 M83318.1 GI:170505
                                                                                                                                                                                                                                      mRNA, partial cds.
                                                                                                                                                                                                                                                      Lycopersicon esculentum 1-aminocyclopropane-1-carboxylate homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                    (bases 1 to 268)
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KDSSHSTEVMNRVHIVYSLSKDGLPGFRVGAIYSNDDVVAAAT"
82 c 58 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
/product=1-aminocyclopropane-1-carboxylate synthase 1B"
/protein_id="AAD30561.1"
/db_xref="GI:4836799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Actinidia chinensis Planch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Actinidia chinensis"
/db_xref="taxon:3625"
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56.5%;
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                     Submitted (11-JUL-1997) Yoshinori Ikoma, National Institute Fruit Tree Science, Department of Citriculture; Okitsu, Shin Shizuoka 424-02, Japan (E-mail:yoshino@kt.affrc.go.jp, Tel:+81-543-69-7111, Fax::81-543-69-2115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikoma, Y., Yano, M. and Ogawa, K. Cloning and expression of genes encoding Acta Horticulturae 398, 179-186 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ethylene-treated fruit cDNA to mRNA.
Actinidia deliciosa
Actinidia deliciosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varidiplantae; Streptophyta; endicotyledons; core endicots;
Spermatophyta; Magnollophyta; endicotyledons; core endicots;
Asteridae; Ericales; Actinidiaceae; Actinidia.
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ACC synthase.
Actinidia deliciosa (sub_species:deliciosa,
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13; Conserv
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AB005722
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 271)
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                     67
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                   //product="ACC synthase"
/protein_id="BAA1157.1"
/db_xref="G1:2275790"
/tanslation="TLTRPELNLLLTFITSKNIHLISDEIYSGTVFSSPDFVSIMEFL
/translation="TLTRPELNLLLTFITSKNIHLISDEIYSGTVFSSPDFVSIMEFL
KDSSHSTEVWNRVHIVYSLSKDLGLPGFRVGAIYSNDDVVLAAAKK"
a 82 c 56 g 66 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="AAA68621.1"
/db_xref="GI:867990"
/translation="LukDTLKSYLSFTNQHNIHLVCDEIYAATVFDTPQFVSIAEILD
EQEMTYCNKDLVHIVYSLSKDMGLPGFRVGIIYSFNDDVVNCARK"
a 58 c 49 g 75 t
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/db_xref="taxon:4081"
/tissue_type="pericarp"
/dev_stage="red ripe fruit"
                                                                                                                                                                                                                /organism="Actinidia deliciosa"
/strain="Hayward"
/sub_species="deliciosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /EC_number="4.4.1.14"
/note="homologue"
                                                                                                                                                                        /db_xref="taxon:3627"
/tissue_type="ethylene-treated fruit"
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56.5%;
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Pred. No. 1.6e
4; Mismatches
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..6e+03;
les 6;
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Direct Submission
Submitted (27-APR-1999) Department of Horticulture, Huajiachi
Submitted (27-APR-1999) Appartment of Horticulture, Huajiachi
Samons. Zhejiang University, Kaixuanlu 268, Hangzhou, Zhejiang
                               1-aminocyclopropane-1-carboxylate synthase; homologue.
Lycopersicon esculentum calyx cDNA to mRNA.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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13; Conserv
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AF146025
Lycopersicon
1 (bases 1 )
                                                                                                                                                          271 bp mRNA linear pLN Lycopersicon esculentum 1-aminocyclopropane-carboxylate homologue mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu,C., Chen,K., Chen,D. and Zhang,S. Molecular cloning of four members of ACC kiwifruit (Actinidia chinensis Planch.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Actinidiaceae; Actinidia.

1. (bases 1 to 271)
                                                                                                                                       M83320.1 GI:170508
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/product="1-aminocyclopropane-1-carboxylate synthase 1A"
/protein_id="Ananoo560.1"
/db_xref="GI:4836797"
/translation="TLTRPELIALLITFITSKNIHLISDEIYSGTVFSSPNFVSIMEVL
KDSSHSTEVWNGVHIYVSGKDLGLPFFRVGAIYSNDDVVVAAAS"

84 c 55 g 65 t
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/db_xref="taxon:3625"
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Pred. No. 1
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1549612
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Oetiker J.H., Olson.D.C., Shiu,O.Y. and Yang,S.F.
Differential induction of seven 1-aminocyclopropane-1-carboxylate
synthase genes by elicitor in suspension cultures of tomato
(Lycopersicon esculentum)
Plant Mol. Biol. 34 (2), 275-286 (1997)
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Yip,W.K., Moore,T. and Yang,S.F.
Differential accumulation of transcripts for four tomato
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Lycopers.con esculentum
Lycopers.con esculentum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Solanaceae; Solanum;
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Differential accumulation of transcripts for four tomato
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<1, .>271
                                                                                     /organism="Lycopersicon
/db_xref="taxon:4081"
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/note="homologue"
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/db_xref="taxon:4081"
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56.5%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnollophyta; Embaceae; Papilionoideae; Vicieae;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-DEC-1994) S.C. Peck, Michigan State University, I
of Energy Plant Research Lab, MSU-DOE Plant Research Lab, East
Lansing, MI 48823, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peck, S.C. and Kende, H. Sequential induction of the ethylene biosynthetic enzymes by indole-3-acetic acid in etiolated peas Plant Mol. Biol. 28 (2), 293-301 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peck, S.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-aminocyclopropane-1-carboxylate synthase; acs2 gene
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                                                                                                                                                                     /Codon_Start=1
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1 EHDTDIECDRNLVHIVYSLSKVMGFPGFRVGIIYSYNDTVVDCTRK"
                                                                                                                                                                                                                                                                                                                                                                                     /gene="ACS2"
<1. .>273
                                                                                                                                                                                                                                                                                                                                              /gene="ACS2"
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Pred. No. 1.6e+03;
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Lycopersicon esculentum.
Lycopersicon esculentum
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Oetiker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F. Differential induction of seven 1-aminocyclopropane-1-carboxylate
                                                                          Lycopersicon esculentum Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; aggonliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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Oetiker, J.H., Olson, D.C., Shiu, O.Y. and Yang, S.F.
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a 55 c 63 g 95 t
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of CDS is an artifact from
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                                                                                                                                                                                                                       GI:1814260
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Pred. No. 1.6e+03;
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Submitted (25-SEP-1996) Vegetable
Submitted Mann Laboratory, Davis,
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Plant Mol. Biol. 34 (2), 275-286 (1997)
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Differential induction of seven 1-aminocyclopropane-1-carboxylate
synthase genes by elicitor in suspension cultures of tomato
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Oetiker, J.H., Olson
                                                                                                                           Direct Submission Submitted (25-SEP-1996) Vegetable Crops, University of California at Davis, Mann Laboratory, Davis, CA 95616, USA
                                                                                                                                                                                   Oetiker, J.H., Olson, D.C.,
                                                                                                                                                                                                                                                        synthase genes by elicitor in suspension (Lycopersicon esculentum)
Plant Mol. Biol. 34 (2), 275-286 (1997)
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                                                                    /organism="Lycopersicon
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/db_xref="taxon:4081"
              /gene="LE-ACS6"
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/EC_number="4.4.1.14"
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/EC_number="4.4.1.14"
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/Codon_statt=1
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SUMMARIES

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Ranu,R.S.
Ranu,R.S.
1-aminocyclopropane-1-carboxylate synthase genes from pelargonium
Patent: US 5824875-A 10 20-OCT-1998;
Location/Qualifiers
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Sequence 10 from patent US
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AF049138 Dianthus
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                                                 697 bp mRNA linear PLN 11-MAR-1998 (ACS2) mRNA, partial cds.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
Dianthus caryophyllus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-JAN-1997) Department of Biological Sciences, Michigan Technological University, Houghton, MI 49931, USA
             Dianthus caryophyllus.
                                        AF049138.1 GI:2947285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="BACS4"
<1. .>621
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/strain="AAA group, cavendish"
/db_xref="taxon:4641"
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/protein_id="AAB47554.1"
/db_xref="GI:1842049"
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Mbeguite-A-Mbeguite,D. and Fils-Lycaon,B.R.
Direct Submission
Submitted (07-SEP-1999) Station de Technologie des Produits
Vegetaux, Institut National de la Recherche Agronomique,
Personaine Saint Paul, Avignon 84914, France
Location/Qualifiers
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Submitted (17-FEB-1998) Horticulture and Landscape Architecture,
Purdue University, 1165 Horticulture, West Lafayette, IN
                                                                                                                                                                                                                                                                                           ACC synthase from apricot fruit Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prunus armeniaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prunus armeniaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prunus armeniaca ACC synthase (ACS1) gene, AF184076
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Differential expression of three members of the ACC synthase gene
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1 (bases 1 to 697)
                                                                                                                                                                                                                                                                                                                                             Molecular cloning and nucleotide sequence of genomic DNA encoding
                                                                                                                                                                                                                                                                                                                                                                     Mbeguie-A-Mbeguie, D. and Fils-Lycaon, B.R.
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GELTLWRVIINEVKINVSPGSSFHCTEPGWFRVCIANMSNDTMEVALRRIRSFVLRIK
DVAKYVVASTKRKCWQTNLQLRLSNKRLDDFWGISQIESPHSASRSIASRSS"
                                        /organism="Prunus armeniaca"
/db_xref="taxon:36596"
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/protein_id="AAC05377.1"
/db_xref="GI:2947286"
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<1. .697
/gene="ACS1"
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2 (bases 1 to 1089)
2 (bases 1 to 1089)
Let.C., Yan, M. and Junping, G.
Direct Submission
Submitted (06-NOV-2001) Ornamental Horticulture and Landscape
Architecture, China Agriculture University, No.2 Yuanmingyuan
Road, Beijing 100094, China
Location/Qualifiers
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Lei,C., Nan,M. and Junping,G.
Cloning of an 1-aminocyclopropane-1-carboxylate cDNA from Rosa cultivar 'Karolinal'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosa hybrid cultivar 'Kardinal'.
Rosa hybrid cultivar 'Kardinal'.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
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Rosa hybrid cultivar 'Kardinal'
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//Codoc_start=1
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/oultivar="Kardinal"
/db_xref="taxon:180465"
/Lissue_type="petals"
1. >>1089
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/gene="ACS1"
/product="ACC synt
join(<1. .35,123.</pre>
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//product="AcC synthase"
/product="AcC synthase"
/protein_id="AcAC16977.1"
//protein_id="AcAC16977.1"
//db_xref="GI:10441265"
//translation="DaffuprpypgidkdikmrTgveIITvpcrsadkfnLsvTallb_fartion="DaffuprpypgidkdikmrTgveIITvpcrsadkfnLsvTallb_farekNiHIISNEE,FAGST_faseRvQAKKGLKVRG_IIISNPSNPVCTLFSRESLYNLLDFAREKNIHIISNEE,FAGST_faseEvSmadiveLedldQnrvHIVvGLSKDLSLpgfragvivSpnkNvLaAAkrLT_fessIsTpSQOLLSSMLSDTKFVQKFLDANREELRGMHLKFLTGLKQLGIECTKSNGG_FSCMADMSGLIRSYNERGELELMDRLINVAKVNVTPGSSCHCIEPGWFRVW"
177 c 204 g 263 t
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/gene="ACS1"
/note="""
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Pred. No. 1.4e+03;
7; Mismatches 5;
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1-aminocyclopropane-1-carboxylate
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RESULT 7
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                  MADU73815 1094
Malus domestica ACC synthase
U73815 GI:1658059
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Capsicum annuum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae, euasterids I; Solanales; Solanaceae; Capsicum.

1 (bases 1 to 1089)

Harpster,M.H., Howie,W. and Dunsmiur,P.

Unpublished

2 (bases 1 to 1089)
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1-aminocyclopropane-1-carboxylate synthase; ACC1
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184 c 245 g 330 t
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/clone="pBetaD1-2"
/cell_line="VS-300"
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1. .1089
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/cultivar="VS-300"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (20-OCT-1994) M.H. Harpster, DNA Plant Technology
on, 6701 San Pablo Avenue, Oakland, California 94608, USA
                                                                                                                                                                                                                                                                                                                                                                66.1%;
47.8%;
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                                                                                                                                                                                                                                                                                                                                    Score 15.2; DB 8;
Pred. No. 1.4e+03;
7; Mismatches 5;
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Pred. No. 1.4e+03;
7; Mismatches 5;
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(MdACS-2) mRNA,
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Malus x domestica

Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Wagnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Malus.

Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-OCT-1996) Food Science & Technology, Cornell University, NYSAES, Geneva, NY 14456, USA
                                                                                                                    Botella, J.R. Ethylene evolution and of mango fruits
                                                                                                                                                                                              Mangifera indica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Anacardiaceae; Mangifera.
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U22523
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11; Conser
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Botella,J.R.
Direct Submission
Submitted (14-MAR-1995) Jose R. Botella, Botany Department,
University of Queensland, John Hines Building, Brisbane, Qu
                                                                                                                                                                                                                                                                                                                       U22523.1 GI:1143811
                                                                                               Unpublished
                                                                                                                                                                                                                                                                               Mangifera indica.
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senfield,C.-L., Kiss,E. and Hrazdina,G.
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/product="ACC synthase"
/product="AAB57988.1"
/protein_id="AAB57988.1"
/db_xref="GI:1658060"
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/translation="QMGLAENQPCFDFRIVMSGGATGAHESLAFCLADPGDAFLVPTP
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#YPGFPRDLRWATGVQLFPVVCESSNNFVTKALEAURIKKAQESTISEVMNEVVGCNDD
IVHIVYSLSKDLGFPGFRYGIIYSYNDVVVNIARKMSSFGLVSTQTQRLIASMLSDTI
FVENFIAKSAMKLSQRHDLFTTGGLGQVEITTLKSNAGLFIWMDLRRFLENSTFDDELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MdACS-2"
/EC_number="4.1.1.14"
/codon_start=1
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171 c 229 g 337 t
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/strain="McIntosh"
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Pred. No. 1.4e+0
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                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Submitted (15-JAN-2002) Institute of Biochemistry, Zhejiang
Submitted (15-JAN-2002) Institute of Biochemistry, Zhejiang Province 310029,
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosaidae; eurosida ; Rosaidae; Rosaidae; Amygdaloideae; Prunus.

1 (bases 1 to 1097).
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                                                                                                                                                                                                                             University, Kaixuan
P. R. China
                                                                                                                                                                                                                                                                                        Yongfeng,J.
                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                      Yongfeng, J. and Yaozhou, Z. Cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                Prunus
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HGLPEFRKAVAKFMGKVRGGRVTFDDDRIVMGGGVTGANEQIIFCLADPGDAELVPSP
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IHIVYSLSKDWGLPGFRYGIVYSYNDAVVSCIRKMSSFGLVSSQTQYLLASMLSDDEF
VEKFLAESSKRLAKRYHIFTKRLEKVGINCLKGNAGLFFWMDLRHLLQQETVDAEMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="fruit"
/dev_stage="mature"
<1. .>1096
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/db_xref="GI:1143812"
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/note="ACC synthase"
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                                                                                                                                                              /organism="Prunus persica"
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VARFLETSSKRLAKRHGVFTKGLEEVGINCLRSNAGLFCWMDLRRLLKDLTFDGEMVI
                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                              ll; Conservative
                 STU70842 1098 bp mRNA linear PLN 17-JJ Solanum (Juberosum 1-aminocyclopropane-1-carboxylate synthase U70842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-NOV-1996) Plant Biology, University of Helsinki, P.O. Box 28 (Viikki 21), Helsinki 00014, Finland Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidop (bases I to 1093)
Vahala, J., Schlagnhaufer, C.D. and Pell, E.J.
Induction of an ACC synthase cDNA by ozone in light-grown Arabidopsis thaliana leaves
Physiol. Flantarum 103, 45-50 (1998)
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U70842.1 $1:2459544
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Spermatchyyta; Magnolliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidorsis thaliana
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                                                                                                                                                                                                                                                                                                                                                   /product="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="AAC32251.1"
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H3LPEFROAVAKFMEKTRINIKVKFDDDRIVMSGGATGAHETVAFCLANPGDGFLVFTP
YYPGFDRDLKWRTGVNLVPVTCHSSNGFKITVSALEAAYENARKSNIPVKGLLVTNPS
WPLGTTIDRECLKSLVWFTNDKGIHLIADEITAATMSGGSETISVAEVLEEIEDCNRD
LIHTVYSLSKUMGLPGLRVGIYVSXNDRVOLARKMSSFLVSSOTGHLIAKMISDES
LYDEUTRESKLRLAARHAEITTGLDGLGIGMLKAKAGLFLWMDLRNLLKTATFDSETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Organism="Arabidopsis thaliana"
|/db_xref="taxon:3702"
| 11. >1008
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265 c 294 g 264 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="ACC synthase; expression is induced by ozone"
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47.8%; Pred. No. .
47.8% 7; Mismatches
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Pred. No. 1.4e+03;
7; Mismatches 5; Indels 0
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1091 CATACTCTAAACCAACCTGGCTC 1069
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Solanum tuberosum
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 1098)
Schlagnhaufer, C.D., Arteca, R.N. and Pell, E.J.
Sequential expression of two 1-aminocyclopropane-1-carboxylate
Synthase genes in response to biotic and abiotic stresses in potato
(Solanum tuberosum L.) leaves
(Solanum tuberosum L.) leaves
(Solanum Mol. Biol. 35 (6), 683-688 (1997)
Jin,Y. and Zhang,Y.

Direct Submission
Submitted (26-FBB-2000) Institute of Biochemistry, Zhejiang
University, Kaixuan Road 268, Hangzhou, Zhejiang 310029, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prunus persica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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Schlagnhaufer,C.D., Arteca,R.N. and Pell,B.J.
Birect Submission
Submitted (16-Sup-1996) Horticulture, Penn Stat
Tyson Building, University Park, PA 16802, USA
                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 1100)
Jin, Y. and Zhang, Y.
                                                                                                                                                                                                                                                              Molecular cloning and expression of peach ACC synthase gene unpublished
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/prodict="1-aminocyclopropane-1-carboxylate synthase"
/protein_id="Anabe880.1"
/protein_i
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LVHIYYSLSKOLGFFGERVGIIYSVRUDVVNIKARQMSSEGLVSTGTGRLIASMISDTI
FVENFIAKSAMKLSQRHDLFTKGLGOVGITTLKSNAGLFIWMDLRRFLENSTFDNELK
LWHIILNKYKLNVSPGCSFLSSEGWFRVCFA*
1 169 c 226 g 341 t
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<1. .>1098
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Pred. No. 1.4e+03;
7; Mismatches 5;
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AF239989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prunus persica.
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                                                                                             Similarity
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LVHIVYSLSKDMGFPGFRVGIVYSYNDAVVNCARKMSSFGLVSTQTQHLIASMLSDND
FVDRFIAQSAKRLKARHMRLTMGLAQVGTSCLKSNGGLFVWMDLKQLLKEQTFEAEMA
LWHTIIHEVKLNVSPGSSFHCPEPGWFRVCFA"
96 a 237 c 280 g 287 t
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                                                                   Conservative
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                                                                                                                                                                                                                 LWRVIINEVKLNVSPGSSFHVTEPGWFRVCFA"
243 c 268 g 292 t
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Pred.
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1091 CACACACGGAACCAACCTGGCTC
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Carica papaya mrNA for 1-aminocyclopropane-1-carboxylate synthase.
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Nucleotide sequence of a cDNA encoding
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Lam, P.F., Tan, C.S. a
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Betula pendula
Betula pendula
                                                                     AY120898
                                                                                    mRNA, partial cds.
                                                                                                      Betula pendula
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                                                  AY120898.1 GI:21954115
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DLIHIIYSLSKOMGFPGFRVGIVYSYNDAVVSCARKMSSFGLVSSQTQYLIASMLADD
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213 c 254 g 309 t
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47.8%;
                                                                                                      1-aminocyclopropane-1-carboxylate synthase
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Pred. No. 1.
                                                                                                                           1101 bp
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Best Local Similarity 47.8
Matches 11; Conservative
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1091 CATACGCGGAACCAAGCCTC 1069
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Vahala, ...
Direct Sulmission
Submitted (12-JUN-2002) Department of Biosciences, University of Submitted (12-JUN-2002) Department of Biosciences, University of Helsinki, Vikinkaari 5D FIN-00014 University of Helsinki, Finland Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vahala, ... Ruonala, R., Keinanen, M., Tuominen, H. and Kangasjarvi, J. Kinetics and signaling of ethylene, jasmonic acid and salicylic acid moculate ozone sensitivity in birch (Betula pendula) Unpublished
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(bases 1 to 1101)
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                                                                                                                                                                                         281
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/db_xref="taxon:3505"
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/gene="ACS2"
                                                                                                                           66.1%;
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Pred. No. 1.4e+03;
7; Mismatches 5;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                       O
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                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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                                                   AZ309427
AW687380
AL751692
   AV410488
                                     Z33841
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AW687380 NE009A03R
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Z33841 AFFS2940 St
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21580 AV32	V379564 AV379564	98038 9520	104732 Zea mays	L063501 Drosophi	L050471 Drosophi	209422 SP_010	M451926 AGENÇ	H517544 BOGBR.	M779146 EST589	I421967 EST532	653915 BOMI	708432 BOHTUŽ	112805 EST587	B1921823 EST541	75348 AU17534	B624474 BB6244	1898099 EST2675	I487009 EST2453	505273 AL50527	F649567 NF0790	AW441375 EST31077	.I485332 EST2436	85399 EST243720	304558 1M0004	B61942 T19L13TR T	18	BO696008 NXPV	94662 EST26	315805 Saf6	98837 EST268280	F276958 GA E	650853 30967	993687 70149	803717 10081	65643 20683	E458995 EST4	8708 EST268151	F112525 EST4401

Q

ACCESSION VERSION RESULT 1 AZ309427/c LOCUS COMMENT SOURCE ORGANISM REFERENCE KEYWORDS DEFINITION TITLE AUTHORS JOURNAL plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genet Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 103)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ramil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

,M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,

and Wright, D., Weiss, R., felding with paired and words from 10th AZ309427 103 bp DNA linear GSS 29-SEP-200 1M0013K07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic cione UUGC1M0013K07 R, DNA sequence. Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 84112, Mouse whole genome scaffolding with paired end reads from 10kb AZ309427.1 GI:10350398 nouse mouse USA GSS 29-SEP-2000

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KEYWORDS
SOURCE
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Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 bp NE009A03RT1F1019 Developing root NF009A03RT 5', mRNA sequence AW687380
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW687380.2 GI:11928221
EST.
barrel medic.
                                                                                                                                                      Medicago truncatula root library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7562116
                                                                                                                                                                                                                                                                      Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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                                                                                       Plant Biology Division
The Samuel Roberts Noble
                                                                                                                                                                                                                          ,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel
                     Tel: 580 221 7317 Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                 Medicago.
                                                                                                                                        Contact:
                                                                                                                                                                                                                                                                                                                           (bases 1 to 128)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pNASMICALLY (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                    Sam Noble Parkway, Ardmore,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
nlpaiva@noble.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

41 c 21 g 25 t
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/clone="UUGC1M0013K07"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                        Paiva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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56.5%;
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Pred. No. 1.4e+03;
4; Mismatches 6;
                                                   Foundation rdmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   root Medicago truncatula
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                                                                                                                                                                                                                                    Roberts Noble Foundation
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana T-DNA flanking genomic survey sequence.
AL751692
AL751692.1 GI:21484190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 768 Std Error: 0.0 Plate: 009 row: A column: 03 Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                      Submitted (17-JUN 2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At3961510. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German the context of the GABI-Kat project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                  ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and We A new Arabidopsis thaliana T-DNA mutagenised population for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS
                                                                                                                                        plant Genomics program designated 'GABI'.
availability can be found at:
http://www.mpiz_koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 198)
Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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note" Vector: Lambda Zap; Total RNA was extract non-nodulated roots of plants grown in 1 mM nitr medium. Samples were taken at four time points (approximately two days, one, two and six weeks germination) representing early seedling growth nitrogen limitation."

a 22 c 20 g 43 t
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/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Developing root"
/tissue_type="root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="NF009A03RT"
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/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-006E12-014808"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                                                                  /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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56.5%;
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Pred. No. 1.5e+03;
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lation (GABI-Kat)
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on line
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RESULT 5
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ORIGIN
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AU092777
AU092777 Rice callus Oryza s
Clone C53537, mRNA sequence.
AU092777
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                                                                                                                                                                                                                                                                      Similarity
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12 Rue du General Zimmer, 67084 Strasbourg Cedex,France
Email: AlABANKWEDCC.U-STRASBG.FR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Arabidopsis thaliana transcribed genome: the GDR cDNA program Unpublished (1996)
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/(lone_lib="Strasbourg-A")
/(lone="Vector: Lambda ZAPII; tissue=sliced leaves of /
/(lone)
A thaliana ecotype columbla; clone_library=Strasbourg-A; Cloning vector: Lambda ZAPII; Physiological condition: Léaves strips incubated 2/3/4 days in liquid culture medium."

84 c 82 g 78 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="FAI88"
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56.5%;
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56.5%;
                                         callus Oryza sativa (japonica cultivar-group) cDNA
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bred. No. 1.8e+03;
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Pred. No. 1.6e+03;
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                                                                                                          Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                          Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S. Generation of 7137 non-redundant expressed sequence tags from a Legume, Lotus japonicus DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                  Lotus japonicus.

Lotus japonicus.

Lotus japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV410488 Lotus japonicus young plants (two-week old) Lotus japonicus young plants (two-week old) Lotus japonicus CDNA clone MWL073e12_r 5', mRNA sequence.
AV410488
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Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrhartoideae;
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                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 428)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Rice callus"
/note="Vector: pElluscript II SK+; Site_1: SalI; Site_2:
NotI; cDNA prepared from rice callus mRNAs by using
cligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
128 c 101 g 57 t 2 others
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="C53537"
/organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MuL073el12_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
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56.5%;
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Pred. No. 1.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 431)
Alcala,J., Vrebalov,J., White,R., van der Hoeven,R.S., Holt,I.E., Liang,F., Hansen,T.S., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Egukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF112525 431 bp mRNA linear EST 18-MAY-2001 EST440115 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG64175 5' sequence, mRNA sequence.
AI898708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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BF112525.1 GI:10942215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: CUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation of ESTs from tomato fruit tissue, breaker stage
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                                                                                                                                                                                                                   /note="Vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4081"
/clone="cLEG41J5"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lycopersicon esculentum"/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="tomato breaker
/tissue_type="Pericarp"
                                                                                                                                                                                                                                                                                                                                                   /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                               /dev_stage="breaker"
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Pred. No. 1.
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Pred. No. 1.9e+03;
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 450
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ies 6;
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                                                                                                                                                                       DB 12;
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Query Match
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Contact: CUGI
Clemson University Genomics Institute
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Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
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Contact: CUGI
                                 Generation of ESTs from tomato fruit tissue, immature green Unpublished (2000)
                                                                                                                                                                       Alcala, J., Vrebalov, J., White, R., van der Hoeven, R.S., Holt, I.E., Liang, F., Hansen, T.S., Craven, M. B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/cultivar="TA496"
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Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 479)
Newman, T., deBruijf., F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohl:Ogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Genes galoge: a summary of methods for accessing results from large-scule partial sequencing of anonymous Arabidopsis cDNA clones Plant Physical 106, 1241-1255 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatojhyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatojhyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eirosids II; Brassicales; Brassicaceae; Arabidopsis.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA.
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N65643 | 479 bp mRNA linear EST 05-JAN-1998 20683 Lambda-PRL2 Arabidopsis thaliana cDNA clone 240L12T7, mRNA
                                                                                                                                                                                                                                                                                                                                                              Lansing, M1:
Tel: 517-353-0854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95148729
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                                                                                                                                                                                                                                                           2:3;3tcn@ibm.cl.msu.edu
ime:r: T7 dye primer.
Location/Qualifiers
/grganism="hrabidopsis thaliana"
/strain="var columbia"
/strain="var columbia"
/strain="var columbia"
/db_xref="fcaxon:3702"
/clone="r240L12T7"
/clone="r240L12T7"
/clone="r240L12T7"
/clone="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/clote="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
/clote="Vector: lambda Zip-Lox; The mRNA Sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note_"vector: pBluescriptSKmCUadapt; Site_1: EcoR1; Site_2: Xhol; Fruit were tagged at 5 dpa (0.5 cm) and harvested at 7 day intervals through 35 dpa. Equal masses of tissue from each stage were combined (including seeds and locules) prior to mRNA isolation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_11b="tomato developing/immature green fruit"
/tissue_type="fruit"
/dev_stage="immature green (5-35 days post-anthesis)"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /'db_xref="taxon:4081"
/'clone="clem5013"
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/cultivar="TA496"
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l. .459
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56.5%;
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Pred. No. 2e+03;
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RESULT 11
BH803717
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AUTHORS
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                                                                                                                  BASE COUNT
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Best Local Similarity 56.9
Matches 13; Conservative
                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 1008103 ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Very probable ligation site of ends cut by single endonuclease. Reverse complemented post-ligation sequence from source sequence. Plate: 1008103 row: 5
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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1008103H01.x1 1008 - RescueMu
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                                                                                                                    /organism="Zea mays"
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/db_xref="taxon:4577"
/clone_lib="1008 - RescueMu Grid I"
/tissue_type="leaf:
/tissue_type="leaf: Vector: RescueMu (engineered from pBlueScript backbone): Site_1: BamHI: Site_2: BgIII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, 90 to the
web
site www.zmdb.iastate.edu and follow the links for
'RescueMu' Scrid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BgIII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
69 a 165 c
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56.5%;
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56.5%;
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lon/Qualifiers
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Score 15.4; DB:
Pred. No. 2e+03;
4; Mismatches
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Pred. No. 2e+03;
4; Mismatches
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SueMu Grid I Zea mays genomic, DNA
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    TITLE
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                                                                 AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Gene Expression MicroArray Unpublished (1999)
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                    AA650853
AA650853.1
                                                                                                                                                                                                                                                                                                 AA650853 505 k
30967 Lambda-PRL2 Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4633 World Parkway Circle, St. Louis, MO 63134, USA Tel: 877-577-2733 Fax: 314-427-3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI933687 496 bp mRNA linear EST 08-SEP-1 701497137 A. thaliana, Ohio State clone set Arabidopsis thaliana cDNA clone 701497137, mRNA sequence.
                                    Newman, T., deBruijn, F.J., Green, P., Keegstra, L., Ohlrogge, J., Raikhel, N., Somerville, S.,
                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                               sequence.
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                                                                                   (bases 1 to 505)
                      and Somerville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the
Arabidopsis thaliana Ohio State clone set."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                      GI:2580945
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56.5%;
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summary of methods for accessing results from
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Pred. No. 26
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                                                               Keegstra, K.,
                                                                                                                                                                                                                                                                                                                       linear
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                                          Thomashow, M.,
                                                            Kende,H.,
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RESULT 14
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BF276958
                                                                                                                                                                            Clemson University
100 Jordan Hall, C
                                                                                                                                                                                                                                                                                    ,D., Wood,T.C., Leslie,A. and An integrated analysis of the of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotys; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 519)
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                                                                                                                                 Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                   Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                        Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium arboreum
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                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                Contact: Wing RA
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                                                                                       il: rwing@clemson.edu
primer: TAATACGACTCACTATAGGG
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                                                                  quality sequence stop:
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/clone="288D2T7"
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/strain="var columbia"
/organism="Gossypium arboreum"
                                            Location/Qualifiers
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399 GEATTTCCAGGATTCAGAGTTGG 421
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: h:tp://www.genome.clemson.edu/orders/index.html
5 prime :sequence.
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1 (base) 1 to 521)

Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, P., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.

Generation of ESTs from tomato carpel tissue Unpublished (1999)

Contact: CDG1

CONTACT

CDG1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="7A496"
/cultivar="7A496"
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/clone="clbD35F22"
/clone="cbD35F22"
/clone="cbD35F22"
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/clone="board ovary, TAMU"
/clone="board ovary, TAMU"
/clone="board ovary anthesis to 5 days post-anthesis"
/clone="board ovary pranthesis to 5 days post-anthesis"
/clab_host="xul-Blue MRF'"
/clab_host="xul-Blue MRF'"
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/clab_host="bull ovar palle MRF'"
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/db_xref="taxon:29729"
/clone="gh_Eb0026C04f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                  67.0%;
56.5%;
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Search completed: March 10, 2003, 06:42:37 Job time : 1343 secs

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Maximim Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater tran or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

FEATURES source	JOURNAL MEDLINE COMMENT	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan 1532-3, Kisarazu, Chiba 292-0812, Japan Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/. Location/Qualifiers 1. 221 /organism="Arabidopsis thaliana" /strain="Columbia"	SIZE SETECTED COMM ITOIDITES DNA Res 7, 175-180 (2000) 20363093 Contact: Erika Asamizu The pirof laborator: for plant fore processor	Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. Alarge scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,088 non-redundant expressed sequence tags from normalized and	thale cress. Arabidopsis thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Spermatophyta; Magnollophyta; eudicotyledons; care eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	AV440166 221 bp mrNA linear EST 14-NOV-2000 AV440166 Arabidopsis thaliana above-ground organ two to six-week old Arabidopsis thaliana cDNA clone APD45d02_f 3', mRNA sequence. AV440166 1 GI:7610522 EST.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB595771 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130005F08 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-45-503-9222
Fax: 81-45-503-9216
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    and Hayashizaki, Y.

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/organism="Mus musculus"
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/dev_stage="two to six-week old"
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/clone="APD45d02_f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 bp mRNA linear EST 21-CNW01PL0232 ITEC CNW Wheat Powdery Mildew Resistant Library Triticum aestivum cDNA clone CNW01PL0232, mRNA sequence. BE401232
                                                                                                                                                                                                                                                                                                                               Contact: Jia J
Key Lab. of Crop Germplasm & Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                     http://wheat.pw.usda.gov/genome
                                                                                                                                                                            Email: jizeng@mlmi.cnc.ac.cn
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bread wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGGARCCAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="C130005F08"
/clone_lib="RIKEN full-length enriched, 16 days embryohead"
/clone="CNW01PL0232"
                   /cultivar="Powdery Mildew Resistant line"
/db_xref="taxon:4565"
                                                                            /organism="Triticum aestivum"
                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                   Resources
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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BM149376/c
LOCUS
                             BASE COUNT
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AUTHORS
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SOURCE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.13;
Best Local Similarity 52.23;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CANANNCKRAASMANCCNRSYTC 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center at Baylo: College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030, USA
Fat: 832-824-4536
Fax: 832-824-4536
Email: C.Ones@txcc.org
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wei,Y., 'Tsang,Y.T.N., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr., Gunaratna, P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F. Pediatri: Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (base. 1 to 342)
Wei.Y., "Sang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM149376.1 GI:17170934
EST.
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342 bp mRNA linear EST 30-NOV-2001 TCAAP2011991 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-H3SC project-TCAA Homo sapiens cDNA clone TCAAP1199, mRNA sequence.

BM149376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan
                          51
/ inte="Wector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; first strand cDNA was primed with an anchored xhor-oligo(dT) primer [5'GAAGGACTCGAGCGGCGCAGGAGGAC(T) vn ] v=A,C,G,T] and then dG tailed. Second strand was primed with a BamH1-dC primer [5'AGAAGGCTGCAGCGCGCAATAATAATAATAATAATAATAAT of ].

Double-stranded cDNA was then digested with BamH1 and xhoI and directionally cloned into the BamH1 and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagacka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of Lingth cDNA by improved biotinylated cap trapper., DNA Res 4: 1, 61-6, Feb 28, 1997)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="mcAap1199"
/clone_lib="Pediatric acute myelogenous leukemia
/clone_Lib="Pediatric acute myelogenous leukemia
/clone_ToAA"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                /:issue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B" tric 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf"
/dev_stage="seedling,
strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="ITEC CNW Wheat Powdery Mildew Resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2; DB 10
Pred. No. 1.9e+03;
7; Mismatches 4
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KEYWORDS
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AQ207050
                                       REFERENCE
AUTHORS
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Z34718
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VERSION
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Source
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 CAAACCCTAAACCATCCGACCTC
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|| | | ::||::| | :::||
75 CAGAGACGGAAGCAGCCCAAGCTC
   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 360)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.
Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S.
                                                                                                                                                                                                                     AQ207050

AQ207050

AQ207050

AQ207050.1 GI:3617620
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Contact: Philipps G., Gigot C.
Gigot Claude / L512
Galoratoire de Biologie Moleculaire des Plant 12 Rue du General Zimmer, 67084 Strasbourg Ced Email: ARABANK@MEDDC.U-STRASBG.FR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNRS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Z34718
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ATT53478 Strasbourg-A Arabidopsis thaliana cDNA clone FAI88 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/strain='ecotype Columbia"
/db_xref='taxon:3702"
/clone='TpA188"
/clone='TpA188"
/clone='TpA188'
/clone='TpA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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Young, J., Zhao, S.,
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rg Cedex,France
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                                                                                                            Euteleostomi;
Holzman,
Adams,M.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Washington
401 Queen Anne Avenue North, Seattle,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                   Marra,M., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI608175 361 bp mRNA linear EST 21-APR-vc83h10.y1 Ko mouse embryo 11 5dpc Mus musculus cDNA clone IMAGE:789667 5' similar to TR:Q63418 Q63418 PROTOCADHERIN 3. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 360.
Location/Qualifiers
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                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lunalyoua; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bassa 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AI608175
                                                                                                MGI:474075
This read is a RESEQUENCE of a previously This read has been verified (found to hit
                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI608175.1 GI:4617342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
                                 Possible reversed clone: similarity on Seq primer: Primer name ambiguous
                                                                           correct orientation)
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quality sequence stop: 161.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli_DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="plate=3242 Col=8 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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47.8%;
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Pred. No. 2e+03;
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                                                          wrong strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
BE353050
                                                                                                                                                                    Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE353050 406 bp mRNA linear E DG1_3_F05.g1_A002 Dark Grown 1 (DG1) Sorghum bicolor
                                                                                                                                                                                                                                                                    An EST database from Sorghum: dark-grown Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                    Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                    sorghum
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                                                                                                                                    sequences have been trimmed below Phred quality 16. The
                                                                             High quality sequence start: High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplified by long-range PCR using Ex Taq polymerase for 18 cycles. The PCR-amplifiable cDNA mixture went through one round of equalization and was digested with Sall/NotI and cloned into the Sall/NotI sites of the pSPORTI plasmid vector (Life Technologies). The library was constructed by Dr. Minoru S. H. Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="11.5dpc"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:789667"
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                             Location/Qualifiers
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RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schur,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watarston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE209956 410 bp mRNA linear EST 04-DEC-2001 Sc37b07.yl Gm-c1039 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-jl0 5' similar to TR:043201 043201 GM-c1039-jl0 5' similar to TR:043201 043201 In-AMINOCYGLOPROPANE-1-CARBOXYLATE SYNTHASE; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soybean.
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: e3t@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further informa
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Langth: 1204 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High qua.ity sequence stop: 409.
Lipcation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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hote-"vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XNoI; This cDNA library was constructed from mRNA isolated from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Ogden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XNoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments were directionally cloned into the EcoRI-XNoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This
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/note="Organ: 5-day-old dark-grown seedlings; Vector:
/ambda Zap; Site_1: xhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
(Clones to be sequenced were prepared by mass excision."
88 c 117 g 96 t
                                                                                                                                                                                                                                                                                                                                                 /:issue_type="whole seedling without cotyledons"
/.ab_host="DH10B"
/.note="Vector: pBluescriptII SK+; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                              /bryanism="Glycine max"
//bb_xref="taxon:3847"
/clone="catoome SysTeMS CLONE ID: Gm-c1039-110"
/clone_lib="Gm-c1039"
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                                     AV820681 RAFL11 Arabidopsis thaliana cDNA clone RAFL11-11-L09 3',
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Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A
EST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
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                                                                                                                                                                                                                                                                                                                                                              /note "Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRRA was made from roots of spring barley variety 'Barke', a high quality malting variety, Roots were grown for two days on filter paper at room temperature Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA); NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp" ambiguities. The maximum length was set to 700 bp"
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a 72 c 110 g 130 t 1 others
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/db_xref="taxon:4513"
/clone="HW07907u"
/clone_lib="Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XLOLR"
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Pred. No. 2.2e+03;
                                                                                                                                                                                                                                                                                Score 15.2; DB 9; Pred. No. 2.2e+03;
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RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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An Arabidopsis full-length CDNA library was constructed essentially
An Arabidopsis full-length CDNA library was constructed with BamHI
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 420)
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                                                                                                                                                                                                                                                                               Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AV808550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV808550 RAFL9 Arabidopsis thaliana cDNA clone
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                      Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
                                                                                                                                                                  Seki,M., Narusaka,M., Ishida,J., Kamiya,A.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
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                                                                                                                                           Arakawa,T., Shibata,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  thale cress.
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                                                                                                     Shinozaki, K
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/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to various treatments (dehydration, cold, high salt, ABA, heat and the cold of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thallana"
/db_xref="taxon:3702"
/clone="RaFL11-11-109"
/clone="taFL11"
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47.88;
Seki
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Pred. No. 2.2e+03;
7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23
                                                                                                                                    rninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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                                                                                                                                                                                                                   Satou, M., Nakajima, M.,
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RAFL09-55-E15 3',
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                                   FEATURES
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Best Local
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                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A2863097 431 bp DNA 13
2M0171003F Mouse 10kb plasmid UUGCIM library
Clone UUGC2M0171003 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0171 row: 0 column: 03
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                         University of Utah (
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                    Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                    plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
                                                                        Class: plasmid ends
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                                                  quality sequence stop: 431
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dehydration (1, 2, 5, 10, 24 hr)
hr) treatments"
101 c 72 g 129 t
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/lab_host="DH10B"
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/db_xref="taxon:3702"
/clone="RAFL09-55-E15"
/clone_lib="RAFL9"
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                                   Location/Qualifiers
/organism="Mus musculus"
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47.8%;
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                                                                                                                                                                                                                                                                                                                                      scaffolding with paired end reads
                                                                                                                                                                                                                           Polymers Research Bldg.,
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Pred. No. 2.2e+03;
7; Mismatches 5
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REFERENCE
AUTHORS
TITLE
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BQ468428/c
LOCUS
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ORIGIN
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Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases | to 455)
2 hang, H. Weschke, W., Michalek, W., Stein, N. and EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Reservals 13, 06466, Gatersleben, Germany
Tel: 039482-5595
Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
BQ468428 |
BQ468428.1
EST.
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Hordeum vulgare
Bordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophi/ta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HM01D16T
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                                                                                   /drganism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/dlone="HM01D16"
/dlone="HM01D16"
/tissue_type="male inflorescences"
/tev_stage="male inflorescences (approx.
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory Mouse DNA Resource
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/db_xref="taxon:10090"
/clone="UgC2M0171003"
/clone_1ib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sex="Male" | Year | Male" | Year | Male | Year | Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/).
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                                                                                                                                                                                                                                                                                           . 455
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47.88;
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Pred. No. 2.2e+03;
7; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                         Email: Szhaoetigr.org
Email: Szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 180 row: N column: 17
Seq primer: SP6
Class: BAC ends.
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha nd Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other, GSSS: RPCI-23-180N17.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
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                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="RPCI-23-180N17"
/clone_lib="RPCI-23"
/sex="Female"
/lab.host="DH10B"
/note-"organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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//lab/host-"XLI0-Gold"
//lab/host-"XLI0-Gold"
//note="Wector: pBluescript SK+; Site_1: EcoRI (5'-end of CDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRIadapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinats is not 100% reliable."
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©.	Search completed: March 10, 2003, 06:42:46 Job time : 1341 secs	QY 1 CANANNCKRAASMANCCNRSYTC 23 :: :: Db 157 CACATACTAAACCACCCCAGCTC 135	Query Match 66.1%; Score 15.2; DB 17; Length 457; Best Local Similarity 47.8%; Pred. No. 2.3e+03; Matches 11; Conservative 7; Mismatches 5; Indels 0; Gaps	

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-08-724-194-9
US-08-171-462-5
US-08-846-826A-1
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US-09-043-627-7
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US-08-255-154D-11
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GGNYTNCCNGGNTTYMGNRTNGG	Similarity 100.0%; Similarity 100.0%	STREET: 315 WEST OAK STREET, CITY: FORT COLLINS STATE: CO COUNTRY: USA ZIP: 80521 ZIP: 80521 MEDIUM TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER: ISM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATENTIN Release SOFTWARE: PATENTIN NUMBER: US7/8 APPLICATION NUMBER: US7/8 TELLING DATE: 01-OCT-1996 CLASSIFICATION INFORMATION: RAME: SANTANGELO. USE REGISTRATION UNUMBER: 31,997 TLECOMMUNICATION INFORMATION: TELEPHONE: (970) 224-3100 DRMATION FOR SEQ ID NO: 9: DUBONATION SEQ ID NO: 9: LECOMMUNICATION INFORMATION: TYPE: NUCLEIC CARACTERISTICS: LENGTH: 23 base pairs TYPE: Nucleic acid STARNDEDNESS: single TOPOLOGY: Linear NAME/KEY: misc_feature LOCATION: 9FOUND(3, 6, 9, 12, OTHER INFORMATION: /note= "") 724-194-9	/087 DER DER E-AN NTH# GEF 3		22444422224		
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US-09-171-482-5
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CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under W098/14465; US5,824,875
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: WOR'D Perfect 6.1
SEQ ID NO 5
LENGTH: 23
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TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
FILE REFERENCE: TAGAWA-ROSE
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                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                              NAME: Nadel Esq., Alan S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Botella, Jose
APPLICANT: Sanewski, Garth
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
FILING DATE: 01-MAY-1996
                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S
TELEPHONE: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: One Commerc
STREET: Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                           NUMBER: US/08/846,826A
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%; Score 15.4; 100.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.30
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                                                                                    8795-11
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US-08-846-826A-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                  TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
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                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
TYPE: nucleic acid
                                                                                                                                                                                REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN
FILING DATE: O1-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Botella, Jose APPLICANT: Sanewski, Gar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/846,826A FILING DATE: 01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Commerce Square, 2005 Market Street, 22nd STREET: Floor
                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
NAME/KEY: CDS
                                                 TOPOLOGY:
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VENTION: NOVEL ACC SYNTHASE GENES FROM PINEAPPLES
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195..961
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103..194
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                                                 linear
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                                  CDNA
                                                               double
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56.5%;
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
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RESULT 6
US-09-043-627-1
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; Sequence 1, Application US/09043627
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US-08-860-577-7
                                                                                                                                                                                                                                                                  ALICANDAL CONTROL OF TABLE 1 A V. NAME: MUELLEY, LISA V. REGISTRATION INTUBER: 38,978
REFERENCE/DOCLEY, NUMBER: SVS31
RELECOMMUNICATION: INFORMATION:
TELEPHONE: 312-616-5460
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACIE; ISTICS:
LENGTH: 994 Eake pairs
TYPE: nucleic acid
STRANDEDNESS: $ingle
                                                                                                                                  Matches
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE PA:-PLID Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/860,577
FILLING DATE:
                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
ATTORNEY/AGENT : NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC
TITLE OF INVENTION: Synthase Genes
                                                                      621 GGTCTTCCGGGTTTTCGAGTTGG 643
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180 N. Stetson, 2 Prudential Plaza, Suite
4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boeshore, Maury L.
Deng, Rosaline Z.
Carney, Kim J.
Ruttencutter, Glen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                 Conservative
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56.5%;
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56.5%;
                                                                                                                               4; Mismatches
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                                                                                                                                           Score 15.4;
Pred. No. 18
                                                                                                                                                                                                                                                                                                                                                                                                SVS3801
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Pred. No. 1
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                                                                                                                                                           DB 2; Length 994;
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                                                                                                                               Indels
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RESULT 7
US-09-043-627-7
Sequence 7, Application US/09043627
Patent No. 6124525
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; LOCATION:
US-09-043-627-1
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6124525
GENERAL INFORMATION:
                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/AU96/00
ETIJING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
ETILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEPAX: 609-924-3036
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanet Circle, Suite 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel.
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
                                                                                                                             APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                   691 GGTCTCCCCGGATTCCGAGTCGG 713
                                     STREET: LV. _
CTTY: Princeton
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TYPE: nucleic acid
STRANDEDNESS: single
                 COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bernstein, Scott N. REGISTRATION NUMBER: 38,827 REFERENCE/DOCKET NUMBER: 35
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                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 56.9
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08540-3662
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                 USA
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1..1080
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02-MAY-1996
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20-SEP-1996
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                        APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION: 609-924-8555
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1096 base pair
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FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PA
FILING DATE: 02-MAY-1996
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FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: AU PN5559
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 20-SEP-1996
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NAME: Bernstein, Scott N
REGISTRATION NUMBER: 38,
                                                                                                     CURRENT APPLICATION DATA:
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PRIOR APPLICATION NUMBER: PCT/AU96/00591
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                    FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                            STATE:
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                                                                 APPLICATION NUMBER: US/09/043,627 FILING DATE: 20-MAR-1998
                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                         COUNTRY:
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les 13; Conserv
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                PCT/AU96/00591
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REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
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PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEPHAX: 609-924-3036
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PRIOR APPLICATION DATA:
APPLICATION UNMERS: AU P
FILING DATE: 02-MAY-1996
ATTORNEY AGENT INFORMATION:
NAME: PRIORIES AND PR
                                                                                                                                                                             FILING DATE: 02-MAY-1996 ATTORNEY/AGENT INFORMATION:
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FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
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LENGTH: 1098 base pairs
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APPLICATION NUMBER: AU PN5559
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CTTY: Princeton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: AU PFILING DATE: 20-SEP-1995
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                             Bernstein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: MATHEWS, COLLINS, SHEPHERD & GOULD P.A. 100 Thanet Circle, Suite 306
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                                                                                                                                         Scott N.
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56.5%;
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Pred. No. 1
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US-09-043-627-3
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US-09-043-627-9
                                                                                                                                                                   TELEFAX: 609-934-3036
INFORMATION FOR SIG ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: lirear
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TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
STREET: 100 Thanet Circle, Suite 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 20-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/043,627 FILLING DATE: 20-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: ISI PC compatible
COMPUTER: ISI PC COMPATIBLE
COMPUTER: OF COMPUTER OF COMPUTER
COMPUTER OF COMPUTER O
                                                                                             MOLECULE TYPE: FEATURE:
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697 GGATTCCCTGGATTTAGAGTTGG 719
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                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bernstein, Scott N. REGISTRATION HUMBER: 38,827 REFERENCE/DOCKET NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                 NAME/KEY:
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13; Consérvative
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56.5%; Pred. No. 18;
tive 4; Mismatches
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LOCATION:
US-08-860-577-1
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                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MUELLER, Lisa V.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1384 base pairs
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Patent No.
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Best Local Similarity
Matches 13; Conserv
                             Matches
                                                       Query Match
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Carney, Kim J.
APPLICANT: Ruttencutter, Glen E.
APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plants Expressing ACC
TITLE OF INVENTION: Synthase Genes
NUMBER OF SEQUENCES: 11
                                                                                                                           FEATURE
                                                                                                                                                                       FEATURE
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                                                                                                                                                                                                                           MOLECULE TYPE:
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STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: II.
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TOPOLOGY: linear
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                                                                                                               NAME/KEY:
                                                                                                                                           LOCATION:
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                                          Local
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                                                                                                                                                                                                 NAME/KEY:
1 GGNYTNCCNGGNTTYMGNRTNGG 23
                           1 Similarity 56.1
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60601
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                                                                                                                                                                                                                                                                 nucleic acid
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Deng, Rosaline Z.
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595..1383
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135..433
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                                         67.0%;
56.5%;
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56.5%;
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                             4; Mismatches
                                         Score 15.4;
Pred. No. 1
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Pred. No. 1
                                             19;
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                                                       DB 2; Length 1384;
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970 GGTCTTCCCGGTTTTCGAGTTGG 992

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US-07-809-457A-8
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORREY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-200(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-378-313-18
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: STO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1703 base pair
                                                             APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
TITLE OF INVENTION: in Plants
UMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LOCATION:
                                  STREET:
                                                   ADDRESSEE:
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nes 13; Conser
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STATE: California
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Missouri
                                E: Monsanto Co. BB4F
700 Chesterfield Village Parkway
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11..1489
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                Louis
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56.5%; Pred. No. 20
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC DOS/MS-DOS
COMPUTER: TEM PC DOS
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Patent No. 5702933
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                  FILING DATE: 26-DEC-1990 ATTORNEY/AGENT INFORMATION: NAME: Hoerner Jr., Denni
                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/809,457
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
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APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
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ZIP: 63198
                                                                                                                                                                                                                                                                                  FILING DATE: 0 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGNYTNCCNGGNTTYMGNRTNGG 23
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Hoerner Jr., Dennis R. RATION NUMBER: 30,914
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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26-DEC-1990
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REGISTRATION NUMBER:

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NUMBER OF DANALY STREET: ADDRESS:
ADDRESSEE: MONDANTO CO. BB4F
SIREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READANDE FORM:
MEDIUM TYPE: Phoppy disk
COMPUTER: IBH PC Compatible
OPERATING SYS:IBH: PC-DGS/MS-DOS
SOFTWARE: Patientin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US91/09437
FILING DATE: 19911217
CLASSIFICATION INMBER: PCT/US91/09437
FILING DATE: 26-DEC-1990
ATTORNEY/ACBUT INFORMATION:
NAME: HOETNEY 1T. Dennis R.
REGISTRATION WUMBER: 30,914
REFERENCE/DOCLET NUMBER: 38-21(10538)A
TELECOMMUNICATION INFORMATION:
TELEPAX: (314)537-6047
INFORMATION FOR SEG ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 be se pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: COUNTER
MOLECULE TYPE: CUNA to mRNA
PCT-US91-09437-8
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TELECOMMUNICATION: 1314)537-6099

TELEPHONE: (314)537-6099

TELEPHONE: (314)537-6099

INFORMATION FOR SEC ID NO: 8:

SEQUENCE CHARACTIFRISTICS:
LENGTH: 1800 Hase pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: GDNA to mRNA
US-08-553-943-8
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PCT-US91-09437-8
                                                                         Query Match 67.0%; Score 15.4; I
Best Local Similarity 56.5%; Pred. No. 20;
Matches 13; Conservative 4; Mismatches
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL THEORY IS APPLICANT:
KIS-10-Fe, Ganesh M.
TITLE OF INVENTION:
GONTROL OF FROM INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

67.0%; Score 15.4; I

Best Local Similarity 56.5%; Pred. No. 20;

Matches 13; Conservative 4; Mismatches
994 GGGTTACCAGGATTTAGAGTCGG 1016
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994 GGGTTACCAG3ATTTAGAGTCGG 1016
                                  1 GGNYTNCCNGGNTTYMGNRTNGG 23
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Search completed: March 10, 2003, 06:44:17 Job time: 53 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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             No.
             Pred. No. is the number of results predicted by chance to have a score greater thin or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cjn2_6/ptodata/1/ina/6A_COMB.seq:*
3: /cjn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cjn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5: /cjn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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1 US-08-78-11-494-1
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1 US-08-78-78-313-26
1 US-08-378-313-26
1 US-08-673-768-1
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Sequence 10, Appli Sequence 7, Appli Sequence 3, Appli Sequence 11, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequenc
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EARLIER APPLICATION NUMBER: PCT/US97/17644, Published under W098/14465; US5,824,875
EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Word Perfect 6.1
SEQ ID NO 6
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09043627 Patent No. 6124525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM
TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES
FILE REFERENCE: TAGAWA-ROSE
                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 3, 5, 6, 15, and 18 OTHER INFORMATION: PCR primer
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LOCATION: 3, 5,
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                                                       APPLICATION NUMBER: AU PI
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                   APPLICATION NUMBER: AU P. FILING DATE: 20-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Botella, Jose Ramon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 That
CITY: Princeton
                                                                                                                                                                                                                                                                                         FILING DATE:
                   NAME: Bernstein, Scott N
REGISTRATION NUMBER: 38,8
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                       20-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.1%; Score 15.2; Di 100.0%; Pred. No. 19;
                                                                                                   AU PN9603
                                                                                                                                                               AU PN5559
                                                                                                                                                                                                                           PCT/AU96/00591
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               38,827
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3573-11US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/09043627 ; Patent No. 6124525
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TELEFAX: 609-924-3036
INFORMATION FOR SEQ ID NO:
                                                                                                               TELEFAX: 609-924-3036 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1088 CAGACTCTGAACCAACCAGGCTC 1066
                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PIFILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: AU PN5559 FILING DATE: 20-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 1
FILING DATE: 20-MAR--
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1096 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 609-924-8555
                               MOLECULE TYPE:
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                                                                                    NAME: Bernstein, Scott N. REGISTRATION NUMBER: 38,8
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/AU96/00591 FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Princeton
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Local Similarity 47.8%;
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TOPOLOGY: li
                                                 TOPOLOGY:
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NAME/KEY: CDS
                                                                                TYPE: nucleic acid
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                                                                                                 LENGTH:
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Pred. No. 4
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US-09-043-627-3
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US-09-043-627-3/c
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US-09-043-627-5
                                                         Query Match

Best Local Similarity 47.8

Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION UMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION UMBER: AU PN5559
FILING DATE: 20-SEP-1995
FILING DATE: 20-SEP-1995
PRIOR APPLICATION UMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTONNEY/AGENT INFORMATION:
NAME: BETISTEN WIMBER: 30-07
                                                                                                                                                                                                                                                                     TELEFAX: 609-924-3036 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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1091 CATACTCTGAACCACCCCGGCTC 1069
1097 CAGACGCTGAACCAGCCAGGTTC 1075
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REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
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SOFTWARE: PatentIn Rela
CURRENT APPLICATION DATA:
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TITLE OF INVENTICN: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ALDRESS:
                                                                                                                                                                                           MOLECULE TYPE: CDNA
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TOPOLOGY: linear
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STREET: 100 THai
CITY: Princeton
                  1 CANANNCKRA \S|MANCCNRSYTC 23
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47.8%;
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47.8%; Pred. No. 40;
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                                                           Pred. No. 40;
7; Mismatches
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                                                                          Score 15.2;
Pred. No. 4
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                                                                                         Length 1104;
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; NAME/KEY:
; LOCATION:
US-08-378-313-18
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US-08-632-598-1/c
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US-08-378-313-18/c
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29 959
REFERENCE/DOCKET NUMBER: 29190-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEPHONE: ..., 404-0792
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Best Local S
Matches 11
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TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARATERISTICS:
LENGTH: 1703 base pairs
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Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
                                                                                                                                                                                                           Sequence 1, Application Patent No. 5886164
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          1 CANANNCKRAASMANCCNRSYTC 23
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1254 CAAACTCGAAACCAACCTGGCTC 1232
                                                                                                                                 APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
                                                                                                             CORRESPONDENCE ADDRESS:
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
                                     STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
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CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 47.8 es 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                           ADDRESSEE:
                                                                                                                                                                                                                               1, Application US/08632598
5. 5886164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: USA
94304-1018
                                                                        E: CUSHMAN DARBY AND CUSHMAN 1100 NEW YORK AVENUE N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
11..1489
                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%;
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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US-09-231-240-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 223:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
TELEFAX: 822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1265 CACACCCTGAACCACCCCGGCTC 1243
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                   ATTORNEY/AGENT INFORMATION: NAME: KOKULIS, PAUL N.
                                                                                                                        CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 47.8 nes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                 FILING DATE:
                                                                                                       APPLICATION NUMBER:
                                                                                                                                                            FILING DATE:
                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                     20005-3918
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                                                                                                                                                                                                                                                                                                                     USA
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47.8%;
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                    223355/SEE50112/US
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Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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RESULT 10
US-07-809-457A-8/c
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                                                                                                                                                                                                                                                                Sequence 8, Application US/07809457A Patent No. 5512466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 6.1
SEQ ID NO 1
LENGTH: 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09171482A Patent No. 6184449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 66.1
Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ranu, Rajinder S.

TITLE OF INVENTION: A 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE GENE FROM TITLE OF INVENTION: ROSA TO CONTROL ETHYLENE LEVELS IN ROSES FILE REFERENCE: TAGAWA-ROSE CURRENT APPLICATION NUMBER: US/09/171,482A CURRENT FILING DATE: 1998-10-19 EARLIER APPLICATION NUMBER: PO-19 EARLIER APPLICATION NUMBER: US/09/17644, Published under WO98/14465; US5,824,87 EARLIER FILING DATE: 1997-Sept-30, Published 1998-April-09; 1996-Oct-01 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        TITLE OF INVENTION: CO
TITLE OF INVENTION: in
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             APPLICANT: Klee, Harry J. APPLICANT: Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                         1628 CAAAACCGGAACCATCCCGGTTC 1606
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ORIGINAL SOURCE:
                                                                      CITY: St.
STATE: Mis
                                      COUNTRY: UZIP: 63198
                                                                                       ADDRESSEE: Monsanto Co. Juliage Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CANANNCKRAASMANCCNRSYTC 23
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                                                                     Missouri
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47.8%;
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47.8%;
                                                                                                                                                                            Control of Fruit Ripening and Senescence in Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15.2;
Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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RESULT 11
US-08-553-943-8/c
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FILING DATE: 36-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOERNEY JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (3+4)537-6099
TELEFAX: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08553943 Patent No. 5702933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
FILING DATE: 06-NOV-1995

PRIOR APPLICATION DATA: 07/809,457

FILING DATE: 17-DEC-1991

APPLICATION NUMBER: US 07/809,457

FILING DATE: 26-DEC-1991

APPLICATION NUMBER: US 07/632,440

FILING DATE: 26-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: HOEINER: JT., Dennis R.

REGISTRATION NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 38-21(10538

TELECOMMUNICATION INFORMATION:

TELLEPONE: (314)537-6099

TELLEFAX: (314)537-6049
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PR PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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|| | | ::|| :| | :::||
1394 CAAACTCGGŁACCACCCTGGCTC 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kiee, Harry J.

APPLICANT: Kishore, Ganesh M.

TITLE OF INVENTION: Control of Fruit Ripening and Senescence TITLE OF INVENTION: in plants
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 180( base pairs
TYPE: NUCLEJC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: INM.PC compatible
OPERATING SYMIPM: PC-DOS/MS-DOS
SOFTWARE: Pattentin Release #1.0, Version #1.25
CURRENT APPLICATION HUMBER: US/07/809,457A
FILING DATE: 19911217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 47.8 es 11; Corservative
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06-NOV-1995
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26-DEC-1990
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                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                 38-21(10538)A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.2;
Pred. No. 43;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-21(10538)A
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RESULT 12
PCT-US91-09437-8/c
; Sequence 8, Application PC/TUS9109437
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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RESULT 13
US-08-724-194-3/c
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PCT-US91-09437-8
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ETLING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
ETLING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOETNET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10538)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
IFENCETH. 1300 hage parts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: 1i; MOLECULE TYPE: US-08-553-943-8
                                                                                                                                 Matches
                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 66.1
Best Local Similarity 47.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pair
                                                               1394 CAAACTCGGAACCACCCTGGCTC 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: //
STREET: //
CITY: St. Louis
CTATE: Missouri
rsA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1394 CANACTCGGAACCACCCTGGCTC 1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CO
TITLE OF INVENTION: in
NUMBER OF SEQUENCES: 1
CORRECTE: CE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Flop
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                             1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: 1i
                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
Output
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CANANNCKRAASMANCCNRSYTC 23
                                                                                                                             ll Similarity 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                             1800 base pairs
                                                                                                                                                                                                          linear
:: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compatible
PC-DOS/MS-DOS
                                                                                                                                            66.1%;
47.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Release #1.0, Version #1.25
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                                                                                                                               7;
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                                                                                                                             Score 15.2;
Pred. No. 43;
7; Mismatches
                                                                                                                                                           DB 5;
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                                                                                                                                                           Length 1800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 4/...
The conservative
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08485107 Patent No. 5767376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08724194
Patent No. 5824875
                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (970) 224-: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HENERAL INFORMATION:
APPLICANT: RANU, RAJI
TITLE OF INVENTION: C
TITLE OF INVENTION: S
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1353 CACACTCTAAACCACCCTGGCTC 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         APPLICANT: STILES, JOHN I.

APPLICANT: NEUPANE, KABI R.

TITLE OF INVENTION: ACC SYNTHASE GENE AND ITS USE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CO
                                                                                                                                                                                                                               ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 MONTGOMERY STREET, SUITE 2200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08 FILING DATE: 01-OCT-1996
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                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                    APPLICATION NUMBER:
                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                  CALIFORNIA
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315 WEST OAK STREET, STE 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%;
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                                                      US/08/485,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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Pred. No. 44;
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US-08-485-107-1
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            δδ
                                                                                                        US-08-724-194-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.1%;
Best Local Similarity 47.8%;
                                             Matches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                           TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1254 CAAACCCTGAACCAGCCAGGTTC 1232
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REFERENCE/DOCKET NUMBER: UH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08
FILING DATE: 01-0CT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: RANU, RATITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 15 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1888 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                  LENGTH: 1945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: FORT COLLINS
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                                                             Local
                                                                                                                                       TOPOLOGY:
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1 CANANNCKRAASMANCCNRSYTC 23
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                                                             Similarity
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315 WEST OAK STREET, STE 701
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(415) 397-8338
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                             66.1%;
47.8%;
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SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN GERANIUMS
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                                             7;
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Pred. No. 4
                                                             Score 15.2;
Pred. No. 4
                                              Mismatches
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                                                                          Length 1945;
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                                              Indels
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                                              0;
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                                              Gaps
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Db 1315 CAAACCGTAIA©CAACCGGCTC 1293

Search completed: March 10, 2003, 06:44:21

Job time: 44 secs

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Post-processing: Minimium Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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23
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//gn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
//gn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
//gn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/cjn2_6/ptodata/1/pubpna/PcT_NEW_PUB.seq:*
/cjn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cjn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length DB	3 ID	Description
ш	15.4	67.(23	10 US-09-776-529A-5	Sequence 5, Appl
c 2	15.4	67.0	748	US-09-7	16,
ω	15.4	67.0	1344	9 US-09-938-842A-1571	1571
C 4	14.4	62.€	274	LO US-09-294-093B-4729	
ζī	14.4	62.6	1506	10 US-09-963-285-9	
0	14.4	62.6	2712	LO US-09-963-285-6	ģ
7	14.4		3289	10 US-09-963-285-8	80
æ	14.4	62.6	4158	10 US-09-963-285-3	ω
9	14.4	62.6	6021	10 US-09-963-285-5	Ģ
10	14.4	62.6	6458	10 US-09-963-285-1	1,
11	14.2	61.7	536	0S-09-974-879-57	57,
12	14.2	61.7	1488	9 US-09-938-842A-1726	20
13	14.2	61.7		10 US-09-822-830A-14	Sequence 14, Appi
14	14.2	61.7	-		542
15	14.2	61.7	2274	10 US-09-921-771-5	Sequence 5, Appli
16	14.2	61.7	14962	10 US-09-764-878-244	244
c 17	14.2	61.7	15849	10 US-09-880-107-2362	2367
c 18	13.8	60.0	363	l0 US-09-864-761-24268	Sequence 24268,
c 19	13.8	200	427	0S-09-925-299-409	Seguence 409. Ann

RESULT 2 US-09-770-149-16/c

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4 4 5 4	43	42	41	40	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	23	22	21	20
13.2	13.2	13.2	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4	13.4			13.8		13.8	13.8
57.4 57.4	57.4	.4	ω	ω	ω	w	W	w	w	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	58.3	60.0	60.0	60.0	60.0	60.0	60.0
1374	1122	375	172637	23632	23632	23626	23626	4486	4486	4485	4485	2093	1985	1743	813	609	451	308	110096	22161	3015	594	574	421
9	9			10		10				12	9	12	10	10	10	10	10	10	10	10	9	10	10	10
US-09-905-173-18 US-09-738-626-186	US-10-060-432-18	US-09-783-590-10488	US-09-805-458A-3	US-09-764-860-941	US-09-764-878-262	US-09-764-860-940	US-09-764-878-261	US-10-014-269-33	US-10-002-974-33	US-10-014-269-1	US-10-002-974-1	US-10-044-090-292	US-09-880-107-3442	US-09-776-529A-1	US-09-974-300-293	US-09-833-381-925	US-09-876-889-320	US-09-867-701-3531	US-09-880-107-1542	US-09-764-847-1020	US-10-161-510-6	US-09-864-761-7563	US-09-864-761-13696	US-09-925-299-409
Sequence 186, Appl Sequence 186, App	Sequence 18, Appl	Sequence 10488, A	Sequence 3, Appli		262,	Sequence 940, App		Sequence 33, Appl	Sequence 33, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 292, App	Sequence 3442, Ap	Sequence 1, Appli	Sequence 293, App	Sequence 925, App	Sequence 320, App	`	Sequence 1542, Ap	Sequence 1020, Ap	Sequence 6, Appli	Sequence 7563, Ap	Sequence 13696, A	Sequence 409, App

ALIGNMENTS

RESULT 1 US-09-776-529A-5

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PRIOR APPLICATION NUMBER: US 09/171,482
PRIOR ETILING DATE: 1998-10-19
PRIOR PRILICATION NUMBER: PCT/US97/17644
PRIOR FILING DATE: 1997-09-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LEGGH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: PCR primer
NAMEXEY: misc_feature
LOCATION: (3), (6), (9), (12), (18), and (21)
COP-176-529A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09776529A
Patent No. US20020083484A1
GENERAL INFORMATION:
APPLICANT: Tagawa Greenhouses, Inc.
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-Aminocyclopropane-1-Carboxylate Synthase Gene From Rosa to
TITLE OF INVENTION: Ethylene Levels In Roses
FILE REFERENCE: Tagawa-Rose
CURRENT APPLICATION NUMBER: US/09/776,529A
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US/08/724,194
PRIOR FILING DATE: 1996-10-01
PRIOR FILING DATE: 1996-10-01
                                                                                         Matches
                                                                                                                                 Query Match
                                                                                                              Local
1 GGNYTNCCNGGNTTYMGNRTNGG 23
                     1 GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                         al Similarity 100.
23; Conservative
                                                                                      67.0%; Score 15.4; D
100.0%; Pred. No. 26;
tive 0; Mismatches
                                                                                                                                    DB 10; Length 23;
                                                                                         0;
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                                                                                         0;
                                                                                         Gaps
                                                                                         0;
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APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
ITILE OF INVENTION: Expressed Sequences of Arabidopsis
ITILE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRY)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (1)...(748)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-16
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-938-842A-1571
  SEQ ID NO 157:
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                   PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                           TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                  APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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                     NUMBER OF SEQ ID NOS: 5379
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617 GGTCTTCCTGGTTTCCGCGTGGG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION
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Kricker, Maja
Slader, Ted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorlach, Jorn
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Allen, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ledford, Brooke L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Application US/09938842A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.0%;
56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15.4;
Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 748;
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SEQ ID NO 9
                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                     APPLICANT:
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QУ

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; NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700354878H1
; NAME/KEY: unsure
; LOCATION: 146, 203, 223
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-4729
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Best Local Similarity
Matches 13; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Arabidopsis thaliana US-09-938-842A-1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SEQ ID NO 4729
LENGTH: 274
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                ; sequence 9, Application US/09963285
; Patent No. US20020090707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-294-093B-4729/c
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Best Local Similarity
Matches 12; Conserva
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                                                                             CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
                 PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: APRIL 21, 1998
NUMBER OF SEQ ID NOS: 6207
COEFTWARDE.
                                                                                                                                                                                                      TITLE OF INVENTION: PROMOTER SEQUENCES FILE REFERENCE: 13425-042001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             APPLICANT: Enerbck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 862 GGTCTTCCTGGTTTCCGCGTGGG 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 GTTTCCCAGGCTTCAGCATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGNYTNCCNGGNTTYMGNRTNGG 23
                                                                                                                                                                                                                                                                   Krook, Katarina
Rondahl, Lena
                                                                                                                                                                                                                                               Wasserman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ito, Laura,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.6%;
54.5%;
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56.5%;
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.4; DB 10;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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GENERAL INFORMATION:

APPLICANT: ENERDCK, Sven
APPLICANT: KROCK, KATARIA
APPLICANT: KROCK, KATARIA
APPLICANT: WASSERTAD, WYETH
TITLE OF INVENTICN: PROMOTER SEQUENCES
FILE REFERENCE: 13425-042001
CURRENT APPLICATION UNMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-01-10
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 24
SOPTWARE: FASTESEQ FOR WINDOWS Version 4.0
SEQ ID NO 6
LENGTH: 2712
         APPLICANT: Enerbel, Sven
APPLICANT: Krook Katarina
APPLICANT: Krook Katarina
APPLICANT: Rondalil Lena
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTIOH: PROMOTER SEQUENCES
FILE REFERENCE: 11425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DAYE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
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US-09-963-285-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (422)...(1903)
US-09-963-285-6
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; LOCATION: (1)...(1503)
US-09-963-285-9
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                                                                                                                                                                                                                                                       Sequence 8, Application US/09963285 Patent No. US2002009D707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.6%;
Best Local Similarity 54.5%;
Matches 12; Conservative
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Best Local :
PRIOR APPLICATION NÚMBER: SE 0003435-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                         1 GGNYTNCCNG:NTTYMGNRTNG 22
|| :| || || || ::| :| |
1214 GGGCTGCCCG:CFTCAGCGTGG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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4; Mismatches
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Pred. No. 1.5e+02;
4; Mismatches 6
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RESULT 9
US-09-63-285-5
; Sequence 5, Application US/09963285
; Sequence 0, Application US/09963285
; Patent No. US20020090707A1
; GENERAL INFORMATION:
APPLICANT: EMERICA, Sven
APPLICANT: KITOOK, KATARINA
APPLICANT: KOOK, KATARINA
APPLICANT: Rondahl, Lena
APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REPERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/09/963,285
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: US 60/238,897
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; NAME/KEY: CDS
; LOCATION: (187)...(1437)
US-09-963-285-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wasserman, Wyeth
TITLE OF INVENTION: PROMOTER SEQUENCES
FILE REFERENCE: 13425-042001
CURRENT APPLICATION NUMBER: US/99/963,285
CURRENT APPLICATION NUMBER: US/09/26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR PPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEO ID NOS: 24
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US-09-963-285-3
I Sequence 3, Application US/09963285
Patent No. US20020090707A1
GENERAL INFORMATION:
APPLICANT: Enerbok, Sven
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-285-8
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.6
Best Local Similarity 54.5
Matches 12; Conservative
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8
LENGTH: 3289
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Best Local Similarity 54.5
Matches 12; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
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|730 GGGCTGCCTGGCTTCAGCGTGG 751
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54.5%;
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Pred. No. 1.7e+02;
4; Mismatches 6
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Pred. No. 1
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L.7e+02;
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; NAME/KEY: exon
; LOCATION: (1649)...(438)
US-09-963-285-5
             US-09-974-879-57

Sequence 57, Application US/09974879

Publication No. US20030028003A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TIFLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: PZ020P2

CURRENT APPLICATION NUMBER: US/09/974,879

CURRENT FILING DATE: 2001-10-12
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; LOCATION: (2235)...(3737)
US-09-963-285-1
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                                                                                                                                                                                    RESULT 11
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: SE 0004102-0
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/238,897
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
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Best Local Similarity
Matches 12; Conserv
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Best Local :
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APPLICANT:
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PRIOR APPLICATION NUMBER: SE 0003435-5
PRIOR FILING DATE: 2000-09-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROMOTER SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Enerbck, Sven
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PRIOR APPLICATION NUMBER: US 60/239,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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nes 12; Conserv
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Wasserman, Wyeth
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54.5%;
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54.5%;
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Pred. No. 1
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6;
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; FEATURE:
NAME/KEY: SITE
LOCATION: (536)
OTHER INFORMATION: n equals a,t,g,
US-09-974-879-57
                             APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US/60/227,866
                                                                                                                                                                                                                                                                                    RESULT 12
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Best Local
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PRIOR FILING DATE: 2000-0: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/066,090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/066,089 FILING DATE: 1997-11-17
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13; Conserv
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56.5%;
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Pred. No. 1.7e+02;
3; Mismatches 7;
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                                                                                                                         PLANTS,
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                                                                                                                             TRANSGENIC PLANTS CONTAINING
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APPLICANT: Genetis Institute, Inc.
APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Gordon G.
APPLICANT: Fecht-21, Kim
APPLICANT: Fecht-21, Kim
APPLICANT: APOSTIND, Michael J.
APPLICANT: Howes Steven H.
APPLICANT: Grahan, James R.
APPLICANT: Grahan, James R.
APPLICANT: Grahan, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: G:N 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT APPLICATION NUMBER: 00195,604
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE 2000-04-06
NUMBER OF SEQ ID NOS: 631
RESULT 14
US-09-954-456-542
US-09-954-456-542
Sequence 542, Application US/09954456
Patent No. US20020115057A1
FERENTI INFORMATION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Sets
FIITLE OF INVENTION: NUMBER: US/09/954.456
CURRENT APPLICATION NUMBER: US/09/954.456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 2099
TYPE: DNA
DRGANISM: Homo stptens
US-09-822-830A-14
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US-09-822-830A-14
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Patent No. US20020142952A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1726
LENGTH: 1488
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Arabicopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                1639 GGGTTTCCAG&CTTGAGAGTGGG 1661
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Pred. No. 1.9e+02;
"""" 7;
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RESULT 15
US-09-921-771-5
US-09-921-771-5
Sequence 5, Application US/09921771
Patent NO. US20020081284A1
Patent NO. US20020081284A1
GENERAL INFORMATION:
APPLICANT: Li, Dean Y.
TITLE OF INVENTION: Manipulation of Arterial-Venous Identity
FILE REFERENCE: 10402-011
CURRENT APPLICATION UMMBER: US/09/921,771
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 6
TYPE: DNA
TYPE: DNA
TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-09-25
PRIOR PELLING DATE: 2000-09-26
PRIOR APPLICATION UNMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR PELLING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
VNMBER OF SEQ ID NOS: 2276
SEQ ID NO 542
LENGTH: 2242
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                           В
                     Search completed: March 10, 2003, 06:46:24
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Job time : 63.5 secs
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Best Local S
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les 13; Conservative
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Pred. No. 2
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